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                                                                                                  May 11, 2004, 16:49:53 ; Search time 54 Seconds (without alignments) 261.618 Million cell updates/sec
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1 KLCERSSGTWSGVCGNNNAC.....QHGSCNYVFPAHKCICYFPC 50
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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σ.	Aay00738 Antifunga	Aab67417 Amino aci	Aab20220 Radish o		Aab61793 White mus	Aar33706 Antifunga		Aaw19280 Raphanus		Aay57564 Wasabia		Adc51222 Brassica	Adc51224 Brassica	Aaw26379 Radish an	Aaw26387 Antifunga	Aaw26389 Antifunga	Aaw26386 Antifunga	Aaw26377 Radish an	Aaw40347 A. thalia
AAW40349	AAY00738	AAB67417	AAB20220	AAB49470	AAB61793	AAR33706	AAR57325	AAW19280	AAW19617	AAY57564	ABP53725	ADC51222	ADC51224	AAW26379	AAW26387	AAW26389	AAW26386	AAW26377	AAW40347
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279	279	279	279	279	279	279	279	279	279	279	279	279	279	277	276	275	274	274	274

## ALIGNMENTS

RESULT 1

Job Howard Jak Antifungal protein; candida; fungal resistance; food additive; radish; crop protection; plant defensin; bacterial protection; preservative. Raphanus sativus antifungal protein 3 (Rs-AFP3). Ā AAW19282 standard; protein; 50 (revised)
(first entry) 25-MAR-2003 21-JAN-1998 AAW19282; AAW19282 

WO9721815-A2

Raphanus sativus.

19-JUN-1997

96WO-GB003068 12-DEC-1996;

95GB-00025455. 96GB-00006552. 13-DEC-1995; 28-MAR-1996;

(ZENE ) ZENECA LTD.

Sijtsma L, Van Amerongen A; Borremans FAM, Rees SB; Puijk WC, Schaaper WMM, , Samblanx GW, Fant F, Broekaert W, S Van Gelder WMJ; Meloen RH,

WPI; 1997-332786/30.

Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.

Disclosure; Fig 1; 65pp; English.

This protein sequence is the Rhapanus sativus (radish) mature antifungal protein (Rs-AFP3), which is homologous to proteins AAW19280- AAW19290. Shorter peptides, based on these proteins have been produced (see AAW19291-92, AAW19294-98, AAW19301-304, AAW19330-34 and AAW31765-834). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease

tolerance of crops, either pre or post harvest. When applied to plants they may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorganism capable of expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct PI field.) 88888888

Sequence 50 AA;

Gaps ö ch 100.0%; Score 301; DB 2; Length 50; 1 Similarity 100.0%; Pred. No. 6.3e-25; 50; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 50; Conserv

1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50

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AAW40350 standard; protein; 50 AA

AAW40350

(first entry) 23-JUN-1998 Radish Rs-AFP3 mature protein domain.

Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene; fungi; radish.

Raphanus sativus

409800023-A2

38-JAN-1998

97WO-GB001672 20-JUN-1997; 96GB-00013753 01-JUL-1996;

(ZENE ) ZENECA LTD.

Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras FRG, Manners JM; Kazan K;

WPI; 1998-086663/08

Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.

Disclosure, Fig 1C; 72pp; English

This sequence represents the radish Rs-AFP3 mature protein domain which is used to explain a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fundi and does not require cytotoxic or potentially harmful chemicals SO CCC CCC X S X X B X X

Sequence 50 AA;

Gaps ó 100.0%; Score 301; DB 2; Length 50; 100.0%; Pred. No. 6.3e-25; Live 0; Mismatches 0; Indels 50; Conservative Local Similarity Query Match Best Loca Matches

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AAB49478 standard; protein; 50 AA (first entry) 07-MAR-2001 AAB49478; 

Radish antifungal protein Rs-AFP3

Radish; antifungal; antimicrobial

Raphanus sativus.

.; 0

WO200071735-A1.

30-NOV-2000

18-MAY-2000; 2000WO-GB001905.

99GB-00011933

21-MAY-1999;

(ZENE ) ZENECA LID.

Greenland AJ, Fuentes Mateos AM,

WPI; 2001-041066/05.

Antimicrobial composition useful for treating microbial diseases in plants, comprises two antimicrobial agents, which are antifungal protein from Radish and Mirabilis of Impatiens.

Disclosure; Page 26; 29pp; English

The present sequence is an antifungal protein from Radish. This protein is useful for treating microbial diseases in plants and for inhibiting microbial growth in foodstuffs. In addition, the present sequence is useful for producing plants with improved resistance to microbial pathogens. The present protein can be used in conjunction with other antimicrobial proteins from Mirabilis (see AAB49472-B49473), and Impatiens (see AAB49474-B49477) to form an antimicrobial composition

Sequence 50 AA;

Gaps ö ch 100.0%; Score 301; DB 4; Length 50; Smilarity 100.0%; Pred. No. 6.38-25; 50; Conservative 0; Mismatches 0; Indels Query Match Best Local Matches 5

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1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC

RESULT 4 AAW26384

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AAW26384 standard; protein; 50 AA AAW26384; 

(first entry) 13-DEC-1997 Radish antifungal protein 2 mutant (delQ1,Q5M/P7S/K30G)

Rs-AFP2; radish antifungal protein 2; fungicide; salt tolerance; preservative; transgenic plant; crop protection.

Raphanus; sativus Synthetic.

; 0

Chimeric.

WO9721814-A1

19-JUN-1997.

96WO-GB003065 12-DEC-1996;

RESULT 3 AAB49478

protein

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AW2371-90) are based on Rs-AFP2 and contain at least 1 mutation selected from a basic residue at positions 9 or 39, and a hydrophobic residue at positions 9 or 39, and a hydrophobic residue at positions 5 or 16. Proteins containing GlnSMet (see AAM26379), GlyjBArg (AAW26376), Val39Arg (AAW26377) or Gly9Arg plus Val39Arg (AAW26376) mutations are specifically claimed. A cDNA clone encoding Rs-AFP2 preprotein can be modified by recombinant DNA methods to allow expression of mutant isoforms in yeast as mating factor alpha 1 antifungal activity, especially when expressed in plant tissue where that may have curative as well as protective effects. They are useful for combating fungal diseases in agricultural, pharmaceutical or preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This polypeptide comprises a mutant isoform of radish antifungal protein (ERS-AFP2) (see also AAM19616). Novel potent antifungal proteins (see AAW26371-90) are based on Rs-AFP2 and contain at least 1 mutation selected from a basic residue at positions 9 or 39, and a hydrophobic residue at positions 5 or 16. Proteins containing GlnSMet (see AAW26379) (Gly16Met (AAW26398), Gly9Arg (AAW26378)) vol199Arg (AAW26378) mutations are specifically claimed. A cDNA clone encoding Rs-AFP2 preprotein can be modified by recombinant DNA methods to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New active mutants of radish antifungal protein 2 - used to gener
fungus-resistant plants or as therapeutic or preservative agents.
                                                this polypeptide comprises a mutant isoform of radish antifungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rs-AFP2; radish antifungal protein 2; fungicide; salt tolerance; preservative; transgenic plant; crop protection.
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                                                                                                                                                                                                                                                                                                                                     Score 294; DB 2; Length 50 Pred. No. 3.5e-24; 0; Mismatches 1; Indels
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                Disclosure; Page 4; 39pp; English.
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                                                                                                                                                                                                                               This polypeptide comprises a mutant isoform of radish antifungal protein 2 (Rs-AFP2) (see also AAM19616). Novel potent antifungal proteins (see AAM2631-90) are based on Rs-AFP2 and contain at least I mutation selected from a basic residue at positions 9 or 39, and a hydrophobic residue at positions 5 or 16. Proteins containing GlnsMet (see AAW26379), Gly9Arg (AAW26380), Gly9Arg (AAW26380), Gly9Arg (AAW26380), Mutations are specifically claimed. A cDNA clone encoding Rs-AFP2 preprotein can be modified by recombinant DNA methods to allow expression of mutant isoforms in yeast as mating factor alpha 1 fusion proteins. The Rs-AFP2 mutants have enhanced salt tolerant antifungal activity, especially when expressed in plant tissue where that may have curative as well as protective effects. They are useful for combaring fungal diseases in agricultural, pharmaceutical or preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rs-APP2, radish antifungal protein 2, fungicide; salt tolerance; (RT) preservative; transgenic plant; crop protection.
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                                                                                                                                                    New active mutants of radish antifungal protein 2 - used to generate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Radish antifungal protein 2 mutant (delQ1,Q5E/P7S/K30G/V39R).
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Pred. No. 3.5e-24;
Mismatches 1; Indels
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                                                                                Broekaert WF,
                13-DEC-1995;
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1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC

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allow expression of mutant isoforms in yeast as mating factor alpha I fusion proteins. The Rs-AFP2 mutants have enhanced salt tolerant antifungal activity, especially when expressed in plant tissue where that may have curative as well as protective effects. They are useful for combating fungal diseases in agricultural, pharmaceutical or preservative applications
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Sequence 50 AA;

ö Gaps ö 50 50 1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC Length 50; ch 97.3%; Score 293; DB 2; Length 50 ll Similarity 98.0%; Pred. No. 4.5e-24; A9; Conservative 0; Mismatches 1; Indels Query Match Best Local S Best Loca Matches qq à

1 KLCERSSRTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC

Radish antifungal protein 2 mutant (delQ1,Q5E/P7S/G16M/K30G)

Rs-AFP2; radish antifungal protein 2; fungicide; salt tolerance; preservative; transgenic plant; crop protection.

Rees SB;

New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents.

This polypeptide comprises a mutant isoform of radish antifungal protein 2 (Rs-AFP2) (see also AAW19616). Novel potent antifungal proteins (see AAW66311-90) are based on Rs-AFP2 and contain at least 1 mutation selected from a basic residue at positions 9 or 39, and a hydrophobic residue at positions 5 or 16. Proteins containing GlnSMet (see AAW26379), GlyBArg (AAW26380), GlyBArg (AAW26376), Val33Arg (AAW26377) or GlyBArg plus Val33Arg (AAW26377) or GlyBArg plus Val33Arg (AAW26379) mutations are specifically claimed. A cDNA clone encoding Rs-AFP2 preprotein can be modified by recombinant DNA mechads to allow expression of mutant isoforms in yeast as mating factor alpha 1 fusion proteins. The Rs-AFP2 mutants have enhanced salt tolerant antifungal activity, especially when expressed in plant tissue where that may have ourative as well as protective effects. They are useful for combating fungal diseases in agricultural, pharmaceutical or preservative 

Length 50; Score 292; DB 2; Pred. No. 5.7e-24; 97.0%; 98.0%; Query Match Best Local Similarity

This polypeptide comprises a mutant isoform of radish antifungal protein 2 (Rs-AFP2) (see also AAW19616). Novel potent antifungal proteins (see AAW26371-96) are based on Rs-AFP2 and contain at least 1 mutation selected from a basic residue at positions 9 or 39, and a hydrophobic residue at positions 5 or 16. Proteins containing GlnSMet (see AAW26379), GlypArg (AAW26380), GlypArg (AAW26376), Val39Arg (AAW26377) or GlypArg plus Val39Arg (AAW26370) mutations are specifically claimed. A cDNA clone encoding Rs-AFP2 preprotein can be modified by recombinant DNA methods to allow expression of mutant isoforms in yeast as mating factor alpha 1 fusion proteins. The Rs-AFP2 mutants have enhanced salt tolerant may have curative as well as protective effects. They are useful for combating fungal diseases in agricultural, pharmaceutical or preservative New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents. Radish antifungal protein 2 mutant (delQ1,Q5E/P7S/G9R/K30G/V39R) Rs-AFP2; radish antifungal protein 2; fungicide; salt tolerance; preservative; transgenic plant; crop protection. 50 1 KLCERSSGTWSGVCWNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC SB; Rees Disclosure; Page 4; 39pp; English. AAW26383 standard; protein; 50 Broekaert WF, De Samblanx GW, 96WO-GB003065 95GB-00025474 (first entry) WPI; 1997-332785/30. (ZENE ) ZENECA LTD. Raphanus; sativus 13-DEC-1995; WO9721814-A1 12-DEC-1996; 13-DEC-1997 19-JUN-1997. Synthetic. Chimeric. AAW26383; RESULT 8 AAW26383 g 

applications

Sequence 50 AA;

Gaps ; 95.0%; Score 286; DB 2; Length 50; 96.0%; Pred. No. 2.5e-23; rive 0; Mismatches 2; Indels Similarity 96.0 Query Match Best Local Si Matches 48;

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50 20

1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 1 KLCERSSRTWSGVCGNNNACKNQCIRLEGAQHGSCNYRFPAHKCICYFPC

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AAW19283 ID AAW1 XX RESULT 9

AAW19283 standard; protein; 51 AA

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Antimicrobial composition useful for treating microbial diseases in plants, comprises two antimicrobial agents, which are antifungal protein from Radish and Mirabilis of Impatiens.
                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is an antifungal protein from Radish. This protein is useful for treating microbial diseases in plants and for inhibiting microbial growth in foodstuffs. In addition, the present sequence is useful for producing plants with improved resistance to microbial pathogens. The present protein can be used in conjunction with other antimicrobial proteins from Mirabilis (see AAB49472), and ministrobial composition ministrobial composition from ministrobial composition and ministrobial composition.
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 26; 29pp; English.
                                                                                                                                                                                                                             Greenland AJ, Fuentes Mateos AM;
                                                                                                                                                     99GB-00011933.
                                                                                                                 18-MAY-2000; 2000WO-GB001905.
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                                                                                                                                                                                                                                                                   WPI; 2001-041066/05.
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                                     WO200071735-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 51 AA;
                                                                                                                                                     21-MAY-1999;
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                                                                           30-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW19281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This protein sequence is the Raphanus sativus (radish) mature antifungal brotein (Rs-AFW), which is homologous to proteins AAM19280- AAM19290. Shorter peptides, based on these proteins have been produced (see AAM19291-92, AAM19291-98, AAM19301-304, AAM19330-34 and AAM1165-834). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease tolerance of crops, either pre or post harvest. When applied to plants may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorganism capable of expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                               Antifungal protein; candida; fungal resistance; food additive; radish; crop protection; plant defensin; bacterial protection; preservative.
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Borremans FAM, Rees SB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 282; DB 2; Length 51;
Pred. No. 6.7e-23;
3; Mismatches 2; Indels
                                                                                           Raphanus sativus antifungal protein 4 (Rs-AFP4).
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Samblanx GW, Fant F,
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                                                                                                                                                                                                                                                                                                     96WO-GB003068
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96GB-00006552.
                                     (revised)
(first entry)
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Broekaert W, Samblam
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Best Local Similarity
Matches 45; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                 (ZENE ) ZENECA LID.
                                                                                                                                                                                       Raphanus sativus.
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28-MAR-1996;
                                   25-MAR-2003
21-JAN-1998
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AAW19283;
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Antifungal protein, candida, fungal resistance, food additive, radish, crop protection, plant defensin; bacterial protection; preservative.
                                                            Gaps
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, Samblanx GW, Fant F, Borremans FAM, Rees SB;
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                                                                                                                                                         2 KLCERSSGTWSGVCGNNNACKNQCINLEGARHGSCNYIFPYHRCICYFPC 51
                                                                                                                      1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
   Length 51;
Match - 93.7%; Score 282; DB 4; Length 51 Local Similarity 90.0%; Pred. No. 6.7e-23; local 45; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raphanus sativus antifungal protein 2 (Rs-AFP2)
                                                                                                                                                                                                                                                                                                                                      AAW19281 standard; protein; 51 AA
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à g WPI; 1997-332785/30.

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This protein sequence is the Rhapanus sativus (radish) mature antifungal protein (Rs-AFP2), which is homologous to proteins AAM19280- AAM19290.

Shorter peptides, based on these proteins have been produced (see AAW19291-92, AAW19294-98, AAW1901-304, AAW1930-34 and AAW1765-834).

Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, they may also have curative as well as protective actions. The peptides to plants they may also have curative as well as protective actions. The peptides microorganism capable of expressing the peptide into the soil. (Updated on 25-WAR-2003 to correct PI field.)
      Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rs-AFP2; radish antifungal protein 2; fungicide; salt tolerance;
preservative; transgenic plant; crop protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Gln at position 5 may be replaced by hydrophobic amino acid, preferably Met""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KLCQRPSGTWSGVGGNNNACKNQCIRLEKARHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                          93.4%; Score 281; DB 2; Length 51; 92.0%; Pred. No. 8.6e-23; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Radish antifungal protein 2 (Rs-AFP2).
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                                                                              Disclosure; Fig 1; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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Gaps

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This polypeptide comprises radish antifungal protein 2 (Rs-AFP2). Novel potent antifungal proteins (see AAW26371-90) based on Rs-AFP2 contain at least 1 mutation selected from a basic residue at positions 9 or 39, and a hydrophobic residue at positions, 5 or 16. Proteins containing Gln5Met (see AAW26379), Gly16Met (AAW26300), Gly2Arg (AAW26376), Val39Arg (AAW26377) or Gly9Arg plus Val39Arg (AAW26376) mutations are specifically claimed. A cDNA chone encoding Rs-AFP2 preprotein can be modified by recombinant DNA methods to allow expression of mutant isoforms in yeast as mating factor alpha 1 fusion proteins. The Rs-AFP2 mutants have enhanced salt tolerant antifungal activity, especially when expressed in plant tissue where that may have curative as well as protective effects. They are useful for combating tungal diseases in agricultural, pharmaceutical or preservative applications
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents an antifungal peptide. The invention relates to an antifungal composition comprising one or more antifungal agents and one or more food additives, providing that the composition does not contain nicin or lactoferrin or a derivative, trichorziamine or lysozyme, the relative amounts of antifungal agent and food additive being such that they enhance the activity of the overall antifungal activity of the composition. Especially the antifungal agent is derived from a plant or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Food additive synergistically enhances activity of an antifungal agent especially for prevent food and beverage spoilage.
                                          New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 51,
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92.0%, Pred. No. 8.6e-23;
ive 2, Mismatches 2, Indels
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                                                                                                      Claim 1; Fig 1; 39pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 92.0%
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Sequence 51 AA;
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                                          Query Match
Best Local S:
Matches 46
                                                                                                                                                                                                                             AAB20221;
                                                                                                                                                                  RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a a plant defensin protein. Defensins have antimicrobial properties. The specification describes a modified Cyscontaining antimicrobial peptide derived from a plant defensin. The peptide is modified by introducing one or more Cys residues and/or form disulfide bridges. The antimicrobial peptide is useful in the treatment and prevention of microbial infections e.g. for combating fungal infection. It is useful for agricultural and pharmaceutical applications. It is also useful for agricultural and pharmaceutical fungal and is also useful in combating bacterial infections. A DNA sequence encoding the antimicrobial peptide is useful for producing transgenic plants with increased resistance to microbial pathogen, such that the plant is used as a parent in standard plant breeding crosses to develop hybrids and lines having improved fungal resistance
seed and the food additive is selected from an acid, salt or ester or a 1 dec alkyl ether or derivatives. The compositions are useful in preventing food spoilage e.g. in a wide range of foods and beverages including fruits, jams and dairy products, caused by the spoilage organisms fruits, jams and dairy products, caused by the spoilage organisms hastriam culmorum, Penicallium chrysogenum, P. roquefortli, P. nalgiovense, P. commune, Alternaria sp., Cladosporum sp., Tichoderma harzianum, Mucor plumbeus, Aspergillus versicolor and Scopulariopsis brevicaulis. The food additive and antifungal agent act synergistically to enhance the overall antifungal activity of the composition to a level above the sum of each single component
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial peptide for combating bacterial infections, comprises modified cysteine residues, modified by addition, substitution or deletion to block their ability to form disulfide bridges.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fant F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Defensin; antimicrobial; microbial infection; fungal infection; pathogenic fungi; bacterial infection; transgenic plant; microbial pathogen; fungal resistance.
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                                                                                                                                                                                                                                                        1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                 Score 281; DB 2; Length 51;
Pred. No. 8.6e-23;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Amerongen A,
                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of the plant defensin Rs-AFP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schaaper WMM, Sijtsma L,
Rees SB, Osborn RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 3; 45pp; English.
                                                                                                                                                                                                                                                                                                                                        AAB67416 standard; protein; 51 AA
                                                                                                                                                                                  93.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99GB-00018156
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Posthuma GA, Schaaper WM
Borremans FAM, Rees SB,
                                                                                                                                                                                                              46; Conservative
                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raphanus sativus
                                                                                                                                                        Sequence 51 AA;
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Val, Leu, Phe, His in antimicrobial protein/peptide of
Claim 1"
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protein/peptide of Claim 1"
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Gln, Lys, Arg, Phe or His in antimicrobial
protein/peptide of Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "optionally substituted by Leu, Ile, Trp, Phe,
Met, Lys, Arg, Tyr or His in antimicrobial
protein/peptide of Claim 1"
                                                                                                             Gaps
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Phe, Lys, Arg, Tyr, Met, Cys or His in antimicrobial
protein/peptide of Claim 1"
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Thr, Tyr, Gln, Asn, Lys, Arg or His in antimicrobial
protein/peptide of Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Radish; defensin; Rs-AFP2; antimicrobial; antifungal; fungicide;
transgenic plant; disease resistance; infection; therapy.
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                                                                                                                                                            1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
                                                                                                                                                                                                     51
                                                                                                                                                                                    Length 51;
                                                               Score 281; DB 4;
Pred. No. 8.6e-23;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                    93.4%;
92.0%;
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                                                                                                                46; Conservative
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21. 45
25. 47
                                                                                          Similarity
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Misc-difference 32
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Disulfide-bond
Disulfide-bond
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Schaaper WMM, Sijtsma L,
31-JUL-2000; 2000WO-GB002941.
                                  99GB-00018155.
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                                                                     (ZENE ) ZENECA LTD.
                                                                                                      Posthuma GA,
Borremans FAM;
                                  02-AUG-1999;
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Van Amerongen A,

Novel antimicrobial proteins derived from plant defensin useful against a broad spectrum of microbes, comprise substitutions at specified portions of its sequence.

Disclosure; Page 6; 64pp; English

The present sequence is that of radish defensin protein Rs-AFP2. A claimed antimicrobial protein or peptide is derived from a plant defensin characterised by having lor more replacement amino acids, as indicated at positions 32, 34, 35, 36, 37, 38, 39, 40, 41 and/or 42 of the Rs-AFP2 sequence, provided that the replacement amino acids are not found raturally at these positions and the protein does not comprise only a replacement arginine at position 37, 39 or 42. In addition, cysteine residues may be replaced by alpha-aminobutyric acid. The antimicrobial protein or peptide is preferably derived from Rs-AFP1 (see AAF2220), Rs-AFP1, Hs-AFP2, Bn-AFP2, Bn-AFP2, Bn-AFP2, Sa-AFP1, Sa-AFP4, Br-AFP9, Dn-AMP1. The antimicrobial protein or peptide can be used on its own, or in synergistic combination with a plant defensin, to combat fungi. A plant having improved resistance to a fungal or microbial pathogen can contain recombinant DNA which expresses a clanked antimicrobial protein or peptide. The claimed antimicrobial protein or peptide is also used as a pharmaceutical to treat or prevent a microbial infection, especially a fungal infection (all claimed) 

Sequence 51 AA;

Gaps ; 0 93.4%; Score 281; DB 4; Length 51; 92.0%; Pred. No. 8.6e-23; tive 2; Mismatches 2; Indels Query Match Best Local Similarity 92.09 Matches 46; Conservative

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a 8

Search completed: May 11, 2004, 16:56:27 Job time : 55 secs

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1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
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ilarity 100.0%; Pred. No. 6.5e-26;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Broekaert, Willem
APPLICANT: Van Gelder, Wilhelmus
APPLICANT: Rees, Sarah
IITLE OF INVENTION: Antifungal Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Samblanx, Genoveva
Sititema, Lolke
Meloen, Robbert
Puijk, Wouter
Schaaper, Wilhelmus
Broekaert, Willem
Van Gelder, Wilhelmus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
Local Sim
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US-09-077-948A-36
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Matches
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67, Appl
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Sequence 69,
Sequence 11,
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Sequence 1
Sequence 1
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Sequence 1
Sequence 4
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1 KLCERSSGTWSGVCGNNNAC.....QHGSCNYVFPAHKCICYFPC
                                                                 May 11, 2004, 16:55:24 ; Search time 23 Seconds
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Cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-077-951-10
US-09-077-951-68
US-09-077-951-67
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US-09-077-951-11
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US-08-077-951-17
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US-08-656-318A-3
US-08-627-706-18
US-08-777-192-19
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Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
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seg length: 200000000
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US-08-956-459-3

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US-09-077-948A-34

US-09-077-948A-34

US-09-077-948A-34

US-09-777-687-49

US-08-777-192-49

US-08-777-192-49

US-08-777-192-49

US-08-777-192-49

US-09-077-951-22

US-09-077-951-65

US-09-077-951-65

US-09-077-951-65

US-09-077-951-65

US-09-077-951-65
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## ALIGNMENTS

July Luc Sequence 10, Application US/09077951

Sequence 10, Application US/09077951

Patent No. 6372888

GENERAL INFORMATION:
APPLICANT: Brockaert, Willem
APPLICANT: Brockaert, Willem
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: PPDS0093
CURRENT APPLICATION NUMBER: US/09/077,951
CURRENT APPLICATION NUMBER: GB 9525474.4
EARLIER PELING DATE: 1999-03-11
EARLIER PILING DATE: 1999-12-13
EARLIER FILING DATE: 1996-12-13
SEALIER PILING DATE: 1996-12-13
SEALIER PILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOOTWARE: PatentIN Ver. 2.0
SEQ ID NO 10
LENGTH: 50 TYPE: PRT ORGANISM: Raphanus sativus KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50 ; Sequence 36, Application US/09077948A; Patent No. 6605698; GENERAL INFORMATION: Van Amerongen, Aart Borremans, Frans Fant, Franky



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Gaps

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Length 50; Indels

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                                                                                                                                                                                                                                                Score 294; DB
Pred. No. 3.7e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaer, willem
APPLICANT: Broekaer, willem
APPLICANT: Broekaer, willem
APPLICANT: Broekaer, willem
APPLICANT: Mees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: PPDS003
CURRENT PILING DATE: 1999-03-11
BARLIER PILING DATE: 1999-03-11
BARLIER FILING DATE: 1995-12-13
BARLIER FILING DATE: 1995-12-13
SOFTWARE: PAPLICATION NUMBER: PCT/GB96/03065
BARLIER FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: De Samblanx, Genoveva
APPLICANT: Brocksert, Willem
APPLICANT: Reces, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REPERENCE: PD50093
CURRENT APPLICATION NUMBER: US/09/077,951
CURRENT FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: PCT/GB96/03065
BARLIER FILING DATE: 1996-12-13
BARLIER FILING DATE: 1996-12-12
BARLIER FILING DATE: 1996-12-13
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
TYPE: PRT
     PCT/GB96/03065
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Patent No. 6372888
GENERAL INFORMATION:
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; Sequence 71, Application US/09077951
; Patent No. 6372888
                  EARLIER FILING DATE: 1996-12-12 NUMBER OF SEQ ID NOS: 77 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 70 LENGTH: 50
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.0%;
Matches 49; Conservative
  EARLIER APPLICATION NUMBER:
EARLIER FILING DATE: 1996-12
                                                                                                                                                  TYPE: PRT; ORGANISM: Raphanus sativus
US-09-077-951-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Raphanus sativus
US-09-077-951-67
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Matches 49; Conserv
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US-09-077-951-67
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 301; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 50; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.7%; Score 294; DB 4; Length 50; 98.0%; Pred. No. 3.7e-25; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Squence 68, Application US/09077951
; Sequence 68, Application US/09077951
; Patent No. 6372888
; GENREAL INFORMATION:
   APPLICANT: De Samblanx, Genoveva
; APPLICANT: Brockaert, Willem
   APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REPERENCE: PPD50093
; CURRENT PILING DATE: 1990-01-11
; EARLIER PILING DATE: 1995-12-13
; EARLIER APPLICATION NUMBER: GB 9525474.4
; EARLIER PILING DATE: 1995-12-13
; BARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver: 2.0
FILE REFERENCE: 109846-257 (SYN-035)
CURRENT APPLICATION WUMBER: US/09/077,948A
CURRENT FILING DATE: 1998-08-07
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1996-02-12
PRIOR FILING DATE: 1996-03-28
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSEQ for Windows Version 4.0
SCENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaart, Willem
APPLICANT: Broekaart, Willem
TITLE OF INVENTION: Antifungal Proteins
FILE REPERENCE: PPD50093
CURRENT FILING DAFE: 1999-03-11
CURRENT FILING DAFE: 1999-03-11
SEALIER APPLICATION NUMBER: GB 9525474.4
EARLIER FILING DATE: 1999-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-077-951-70
; Sequence 70, Application US/09077951
; Patent No. 6372888
                                                                                                                                                                                                                                                                                                                           TYPE: PRT; CRGANISM: Raphanus sativus
US-09-077-948A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Raphanus sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Conservative
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SEQ ID NO 68 TYPE: PRT

Query Match Matches

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1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KLCERSSGTWSGVCGNNNACKNQCINLEGARHGSCNYIFPYHRCICYFPC 51
                                           2 KLCERSSGTWSGVCGNNNACKNOCINLEGARHGSCNYIFPYHRCICYFPC 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.7%; Score 282; DB 4; Length 51; Best Local Similarity 90.0%; Pred. No. 7.4e-24; Matches 45; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSE: Intellectual Property Group of ADDRESSES: FILLSBURY MADISON & SUTRO LLP STREET: 1100 New York Avenue, N.W. CITY: Washington Avenue, N.W. COUWIRY: U.S.A. STATE: D. C. COUWIRY: U.S.A. ZIP: Z0005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 109846-257(STN-035)
FILE REFERENCE: 109846-257(STN-035)
CURRENT APPLICATION WUMBER: US/09/077,948A
CURRENT APPLICATION WUMBER: US/09/077,948A
FRIOR APPLICATION NUMBER: PCT/CB96/03068
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-18
PRIOR FILING DATE: 1996-12-18
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 141
SOUTHARE: FRALESQ for Windows Version 4.0
SEQ ID NO 37
                                                                                                                                                                 ; Sequence 37, Application US/09077948A; Patent No. 6605698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08656318A; Patent No. 5750594; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                De Samblanx, Genoveva
Sitiram, Lolke
Maloen, Robbert
Puijk, Wouter
Schaaper, Willelmus
Broekaert, Willem
Van Gelder, Wilhelmus
                                                                                                                                                                                                                                             Van Amerongen, Aart
Fant, Franky
                                                                                                                                                                                                                                                                                              Borremans, Frans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; CRGANISM: Raphanus sativus
US-09-077-948A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sarah
                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                 US-09-077-948A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-656-318A-4
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APPLICANT:
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                                                                                                                                                                      1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
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                                                                       Score 292; DB 4; Length 50;
Pred. No. 6e-25;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 286; DB 4;
Pred. No. 2.7e-24;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                               US-09-07-07-91-95
Sequence 69, Application US/09077951
Fatent No. 637288
GENERAL INFORMATION:
APPLICANT: Be amblanx, Genoveva
APPLICANT: Broekaert, Willem
APPLICANT: Broekaert, Willem
APPLICANT: Rees, Sarah
FILE REFERENCE: PDDS003
CURRENT APPLICATION NUMBER: US/09/077,951
CURRENT FILING DATE: 1999-03-11
EARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1995-12-13
SOFTWARE: PELLING DATE: 1995-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PERLING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
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ENGTHALS
SOFTWARE: PATENTING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
ENGTHALS
SOFTWARE: PATENTING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
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CURRENT FILING DATE: 1993-03-11
EARLIER PEDICATION NUMBER: GB 9525474.4
EARLIER PILING DATE: 1995-12-13
EARLIER APPLICATION NUMBER: PCT/GB96/03065
FRARLIER FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.0
; SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaart, Willem
APPLICANT: Rees, Sees, TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: PPD50093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09077951
Patent No. 6372888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%;
Local Similarity 96.0%;
nes 48; Conservative (
                                                                       Query Match
Best Local Similarity 98.0%;
Matches 49; Conservative
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Best Local Similarity 90.03
Matches 45; Conservative
; ORGANISM: Raphanus sativus
US-09-077-951-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Raphanus sativus
US-09-077-951-69
                                                                                                                                                                                                                                                                                                                     US-09-077-951-69
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Gaps

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COMPUTER: CILLEBURY MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 0.0005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICTOSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/56,459
FILING DATE: 12-OCT-1996
CLASSIPFCATION: 80
FILING DATE: 12-OCT-1996
FILING DATE: 12-OCT-1996
FILING DATE: 12-DCT-1996
FILING DATE: 12-DCT-1996
FILING DATE: 12-DCT-1994
FILING DATE: 13-DEC-1994
FILING DATE: 24-DEC-1994
FILING DATE: 24-DEC-1993
FILING DATE: 24-DEC-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CANCUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
UNMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08956459
Patent No. 5919918
                    SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 92.0
Matches 46; Conservative
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                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-627-706-19
                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 46; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-956-459-4
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US-08-627-706-19

Sequence 19, Application US/08627706

Patent No. 5773696

GENERAL INFORMATION

APPLICANT: Shah, Dilip M.

APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Yonnie S.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F

STREET 700 Chesterfield Village Parkway No. 5773696th

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63198

COMPUTER PILS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 281; DB 1; Length 51;
Pred. No. 9.4e-24;
2; Mismatches 2; Indels
OUTTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 436
ATTORNEY/AGENT INFERMATION:
NAME: Cohen, Charles B.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10700) A
TELECOMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
TELEPHONE: (314)537-6047
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 92.0%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rs-AFP2
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Gaps Gaps .. 0 1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50 1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50 2 KLCQRPSGTWSGVCGNNNACKNQCIRLEKARHGSCNYVFPAHKCICYFPC 51 2 KLCQRPSGTWSGVCGNNNACKNQCIRLEKARHGSCNYVFPAHKCICYFPC 51 93.4%; Score 281; DB 2; Length 51; 92.0%; Pred. No. 9.4e-24; tive 2; Mismatches 2; Indels ch 1. Similarity 92.0%; Pred. No. 9.4e-24; 46; Conservative 2; Mismatches 2; Indels ò d

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Search completed: May 11, 2004, 16:59:12 Job time: 42 secs
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-951-9
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Best Local Similarity (
                                                                                       Query Match
Best Local Similarity
Matches 46; Conserv
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                                                                                  GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Sosnberger, Cindy A.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi, UNMBER POR ADDRESS: 20 CORRESPONDENCE ADDRESS: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
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Pred. No. 9.4e-24;
2; Mismatches 2; Indels
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ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRATION SYSTEM: PATENTIN BATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION NUMBER: 34,565
REGISTRATION NUMBER: 34,565
REGISTRATION NUMBER: 38-21 (10700) A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (314) 537-624
TELEFRAX: (314) 537-624
TELEFRAX: (314) 537-624
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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US-09-077-91-9
Sequence 9, Application US/09077951
Sequence 9, Application US/09077951
Sequence 9, Application US/09077951
Settle No. 637288
GENERAL INFORMATION:
APPLICANT: Broekaert, Willem
APPLICANT: Rees, Sarah
ITILE OF INVENTION: Antifungal Proteins
FILE REFERENCE: PDES0093
CURRENT APPLICATION NUMBER: US/09/077,951
CURRENT APPLICATION NUMBER: 1999-0.11
EARLIER PLING DATE: 1999-0.15
EARLIER PLING DATE: 1995-12-13
EARLIER PLING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGIH: 51
                       US-09-103-489-19
; Sequence 19, Application US/09103489
; Patent No. 6215048
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Best Local Similarity 92.0%;
Matches 46; Conservative 2
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                                                                                        1 KLCERSSGTWSGVCGNNNACKNOCIRLEGAQHGSCNYVFPAHKCICYFPC
      Length 51;
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                                             2; Indels
93.4%; Score 281; DB 4;
illarity 92.0%; Pred. No. 9.4e-24;
Conservative 2; Mismatches 2;
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illarity 92.0%; Pred. No. 9.4e-24;
Conservative 2; Mismatches 2.
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US-09-077-951-20

| Sequence 20, Application US/09077951
| Patent No. 637288
| GENERAL INFORMATION:
| APPLICANT: De Samblanx, Genoveva
| APPLICANT: Rees, Sarah
| TITLE OF INVENTION: Antifungal Proteins
| FILE REFERENCE: PDP50093
| CURRENT APPLICATION NUMBER: US/09/077,951
| CURRENT APPLICATION NUMBER: GB 9525474.4
| EARLIER APPLICATION NUMBER: GB 9525474.4
| EARLIER PILING DATE: 1995-12-13
| EARLIER PILING DATE: 1995-12-13
| FARLIER PILING DATE: 1995-12-12
| NUMBER OF SEQ ID NOS: 77
| SOFTWARE: PatentIN Ver. 2.0
| SEQ ID NO 20
| LENGTH: 51
| TYPE: PRT
| GROANISM: Raphanus sativus
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Sequence 37, Appl Sequence 37, Appl Sequence 39, Appl Sequence 21, Appl Sequence 19, Appl Sequence 19, Appl Sequence 18, Appl Sequence 18, Appl Sequence 34, Appl Sequence 34, Appl Sequence 33, Appl Sequence 33, Appl Sequence 36, Appl Sequence 20, Appl Sequence 22, Appl

Sequence 75, Appl Sequence 17, Appl Sequence 23, Appl

ALIGNMENTS

Sequence

Sequence 65, p Sequence 31, p Sequence 39, p Sequence 73, p Sequence 28, p Sequence 28, p

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentur Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
3 US-10-006-252A-37

US-10-072-809A-34

US-09-759-584-59

US-09-759-584-19

US-09-732-561-19

US-09-732-81A-18

US-09-732-81A-18

US-09-732-81A-18

US-10-681-972-18

US-10-681-972-18

US-10-681-972-18

US-10-05-252A-33

US-10-072-809A-35

US-10-006-252A-65

US-10-006-252A-44

US-10-006-252A-44

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US-10-006-252A-45

US-10-006-252A-44
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APPLICANT: Thomma, Bart
APPLICANT: Terras, Franky
APPLICANT: Perninckx, Iris
APPLICANT: Manners, John
APPLICANT: Razan, Kemal
APPLICANT: Rockaert, Willem
ITITE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZEBECA AG Products
STREET: Nilmington
CITY: Wilmington
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INPORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
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Patent No. US20020035738A1
       USA
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STATE:
          Sequence 36, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 69, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
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Sequence 20, Appl
Sequence 20, Appl
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                                                                                                                                                                               May 11, 2004, 16:56:34 ; Search time 42 Seconds (without alignments) 330.437 Million cell updates/sec
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1 KLCERSSGTWSGVCGNNNAC......QHGSCNYVFPAHKCICYFPC
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15: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
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                                      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-10-388-361A-35
US-10-006-252A-9
US-10-006-252A-20
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Maximum DB
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                                             APPLICANT: Broekaert, Willem APPLICANT: Rees, Sarah TITLE OF INVENTION: Antifungal Proteins TITLE PERENENCE: SYN-034DV CURRENT FILING DATE: 2001-12-04 CURRENT FILING DATE: 1998-06-10 PRIOR APPLICATION NUMBER: 09/077,951 PRIOR PRIOR APPLICATION NUMBER: 1996-06-10 PRIOR FILING DATE: 1996-12-12 PRIOR PILING DATE: 1996-12-12 PRIOR FILING DATE: 1996-12-12 PRIOR P
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Sequence 68, Application US/10006252A

Publication No. US20020152498A1

GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaert, Willem
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYN-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT PPLICATION NUMBER: US/10/006,252A
CURRENT PLING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: GB 9525474.4
PRIOR APPLICATION NUMBER: GB 9525474.4
PRIOR APPLICATION NUMBER: PCT/GB96/03065
PRIOR APPLICATION NUMBER: PCT/GB96/03065
PRIOR PILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-12

NUMBER: OF SEQ ID NOS: 77

SEQ ID NO 68
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US-10-006-252A-70
Sequence 70, Application US/10006252A
Sequence 70, Application No. US20020152498A1
GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Receatt, Willem
APPLICANT: Receatt, Willem
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; ORGANISM: Raphanus sativus
US-10-006-252A-10
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ORGANISM: Raphanus sativus
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Matches 49; Conservative
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REFERENCE/DOCKET NUMBER: PPD 50165/UST
FELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1659
FILEPHONE: (302) 886-1659
FILEPHONE: CRRACTERISTICS:
FINDORMATION FOR SEQ ID NO: SEQUENCE CHRACTERISTICS:
FINDORMATION FOR SIGNIO acids
FIRANDEDINESS: single
FORECULE TYPE: protein
FORECULE TYPE: PROTEI
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APPLICANT: BOTTEMANS,
APPLICANT: BOTTEMANS, Genoveva
APPLICANT: Bitlstam, Lolke
APPLICANT: Sitlstam, Lolke
APPLICANT: Meloen, Robbert
APPLICANT: Brockart, Wilhelmus
APPLICANT: Brockart, Wilhelmus
APPLICANT: Nees, Sarah
TILE COF INVENTION: Antifungal Proteins
FILE REPERRNCE: 50034PPDDIV
CURRENT APPLICATION NUMBER: US/10/388,361A
CURRENT FILING DATE: 1996-08-07
PRIOR PILING DATE: 1996-08-07
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-012-12
PRIOR FILING DATE: 1996-012-12
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-012-13
NUMBER OF SEQ ID NOS: 141
SCOTTARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: SO
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Publication No. US20030226169A1
GENERAL INFORMATION:
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APPLICANT: Fant, Franky
APPLICANT: Borremans, Frans
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CRGANISM: Raphanus sativus
US-10-388-361A-36
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RESULT 3
US-10-006-252A-10
Sequence 10, Application US/10006252A
Publication No. US20020152498A1
GENERAL INFORMATION:

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Pred. No. 9.5e-26;
0; Mismatches 1;
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95.0%; Score 286; DB 13;
Best Local Similarity 96.0%; Pred. No. 4.5e-25;
Matches 48; Conservative 0; Mismatches 2;
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         CURRENT FILING DATE: 2001-12-04

PRIOR APPLICATION NUMBER: 09/077,951

PRIOR FILING DATE: 1998-06-10

PRIOR FILING DATE: 1995-12-13

PRIOR APPLICATION NUMBER: GB 9525474.4

PRIOR APPLICATION NUMBER: PCT/GB96/03065

PRIOR PILING DATE: 1995-12-13

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PATCHIN VEr. 2.0
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De Samblanx, Genoveva
Sititema, Lolke
Meloen, Robbert
Puijk, Wouter
Schaaper, Wilhelmus
Broekaert, Willem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.0%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Raphanus sativus
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US-10-006-252A-69
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US-10-006-252A-69
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 97.7%; Score 294; DB 13; Length 50; Similarity 98.0%; Pred. No. 5.7e-26; 49; Conservative 0; Mismatches 1; Indels
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Pred. No. 7.3e-26;
0; Mismatches 1; Indels
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Publication No. US20020152498A1
GENERAL INFORMATION:
APPLICANT: Broekaert, Willem
APPLICANT: Broekaert, Willem
APPLICANT: Rees, Sarah
ITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYN-034DV UNDER: US/10/006,252A
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 2001-12-04
PRIOR PILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-12-13
PRIOR FILING DATE: 1995-12-13
PRIOR FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PATENTIN VET. 2.0
SERVINE: PATENTIN VET. 2.0
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYN-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/077,951
PRIOR APPLICATION NUMBER: 09 525474.4
PRIOR APPLICATION NUMBER: GB 9525474.4
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-12-13
PRIOR FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PATENT OFFE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
LENGTH: 50
LENGTH: 50
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Publication No. US20020152498A1
GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Rees, Sarán
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYN-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.3%;
98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-006-252A-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Raphanus sativus
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Best Local Similarity 98.0
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 49; Conserv
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US-10-006-252A-71
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Pred. No. 1.3e-24;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 282; DB 12;
Pred. No. 1.3e-24;
3; Mismatches 2;
                                                        CURRENT FILING DATE: 2003-03-13
CURRENT FILING DATE: 2003-03-13
PRIOR APPLICATION NUMBER: US 09/07,948
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1996-07
PRIOR FILING DATE: 1996-12-12
PRIOR PLING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
SOFTWARE: FELSE 1996-12-13
SOFTWARE: FELSE 1996-12-13
SOFTWARE: FELSE 10 NOS: 141
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DS-10006252A

Publication No. US20020152498A1

GENERAL INFORMATION:

APPLICANT: De Samblanx, Genoveva

APPLICANT: Brockaert, Willem

APPLICANT: Rees, Sarah

TITLE OF INVENTION: Antifungal Proteins

FILE REFERENCE: SYN-034DV

CURRENT APPLICATION NUMBER: US/10/006,252A

CURRENT PILING DATE: 2001-12-04

PRIOR FILING DATE: 1998-06-10

PRIOR FILING DATE: 1998-06-10

PRIOR PILING DATE: 1998-06-10

PRIOR PILING DATE: 1998-06-10

PRIOR PILING DATE: 1998-12-13

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PETENTION NUMBER: CO SEQ ID NOS: 77

LENGTH: 51

LENGTH: 51
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: S0094PPDDIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Liang, Jihong Shah, Dilip M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 93.7%;
Best Local Similarity 90.0%;
Matches 45; Conservative
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Best Local Similarity 90.0%;
Matches 45; Conservative
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US-10-006-252A-11
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US-10-388-361A-37
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## Sequence 19, Application US/10681972

| Sequence 19, Application US/20040064850A1
| Publication No. US20040064850A1
| GENERAL INFORMATION:
| APPLICANT: Liang, Ulhong
| APPLICANT: Shah, Dilip M. APPLICANT: Shah, Dilip M. APPLICANT: Rosenberger, Cindy A. APPLICANT: Rosenberger, Cindy A. APPLICANT: Rosenberger, Cindy A. APPLICANT: Rosenberger, Cindy A. TITLE OF INVENTION: Plant Pathogenic Fungi
| TITLE OF INVENTION: NUMBER: US/0/681,972
| CURRENT FILING DATE: 2003-10-09
| PRIOR APPLICATION NUMBER: US/09/829,381D
| PRIOR APPLICATION NUMBER: 09/103,489
| PRIOR FILING DATE: 1998-06-24
| NUMBER OF SEQ ID NOS: 20
| SEQ ID NOS: 20
| SEQ ID NO 19
| LEAR OF THE PATHOR OF THE PATHOR OF THE PATHOR PILING DATE: 1998-06-24
| SEQ ID NO 19
| LEAR OF THE PATHOR OF THE PATHOR OF THE PATHOR PILING DATE: 1998-06-24
| SEQ ID NO 19
                                                                                                                                NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
CONTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
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Wu, Yonnie S.
Rosenberger, Cindy A.
ROSENDERION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REALISE FORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,391A
FILING DATE: 09-Apr-2001
CLASSIFICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: COhen, Charles E.
REGISTRATION NUMBER: 34,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 93.4%; Score 281; DB 9; Length 51; Best Local Similarity 92.0%; Pred. No. 1.7e-24; Matches 46; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMUNIVICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEPAX: (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-829-381A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
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Gaps

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1 KLCERSSGTWSGVCGNNNACKNOCIRLEGAQHGSCNYVFPAHKCICYFPC 50
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                                                                                                                                                                                                          Score 281; DB 13; Length 51;
Pred. No. 1.7e-24;
2; Mismatches 2; Indels
  PRIOR APPLICATION NUMBER: PCT/GB96/03065
PRIOR FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 9
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: May 11, 2004, 17:00:01
Job time : 56 secs
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Best Local Similarity 92.0%;
Matches 46; Conservative
                                                                                                                          TYPE: PRT
ORGANISM: Raphanus sativus
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Pred. No. 1.7e-24;
2; Mismatches 2; Indels
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Pred. No. 1.7e-24;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REPERRNCE: 50094PPDD1V
CURRENT APPLICATION NUMBER: US/10/389,361A
CURRENT FILING DATE: 2003-03-13
PRIOR PILING DATE: 1998-08-07
PRIOR PILING DATE: 1996-02-2
PRIOR FILING DATE: 1996-03-28
PRIOR FILING DATE: 1996-03-28
PRIOR PLING DATE: 1996-03-28
PRIOR PLING DATE: 1996-03-28
PRIOR PLING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 141
NUMBER OF SEQ ID NOS: 141
SEQ ID NO 35
LENGTH: SE
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Publication No. US20020152498A1
GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaert, Willem
APPLICANT: Rees, Sarah
ITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYN-034DV
CURRENT FAPPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/077,951
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                         Sequence 35, Application US/10388361A
Publication No. US20030226169A1
                                                                                                                                                                                                                                                                                                                                                                                           Borremans, Frans
De Samblanx, Genoveva
Sitjtsma, Lolke
Meloen, Robbert
Pujk, Wouter
Schaaper, Wilhelmus
Broekaert, Willem
Van Gelder, Wilhelmus
Rees, Sarah
                                                             Query Match
Best Local Similarity 92.0%;
Matches 46; Conservative
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Best Local Similarity 92.0%;
Matches 46; Conservative 2
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; ORGANISM: Raphanus sativus
US-10-681-972-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-388-361A-35
                                                                                                                                                                                                                                                                   US-10-388-361A-35
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US-10-006-252A-9
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APPLICANT:
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                                                                                                                                                                                                                                                                2 KLCQRPSGTWSGVCGNNNACKNQCIRLEKARHGSCNYVFPAHKCICYFPC 51
                                                                                                                                                                                                                       / Match 93.4%; Score 281; DB 13; Length 51; Local Similarity 92.0%; Pred. No. 1.7e-24; les 46; Conservative 2; Mismatches 2; Indels
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Gaps

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0; Indels

Query Match
100.0%; Score 301; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 50; Conservative 0; Mismatches 0;

Length 79;

ઠે g RESULT 2 T07917

.; 0

Gaps

; 0

Length 79;

Query Match
100.0%; Score 301; DB 2; Length 7:
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 50; Conservative 0; Mismatches 0; Indels

artifugal protein - rape (Species: Brasica napus (rape) (Spacession: T07917 (Space

Description	antifungal protein				3]	ar	protein T4012.7 [i	probable antifunga	hypothetical prote	defensin AMP1 - Da	antifungal protein	anther-specific pr	antifungal protein	defensin AMP1 - Cl	antifungal protein		antifungal protein	114	antifungal protein		probable antifunga	probable gamma-thi	anther-specific pr	pit1 protein (clon	gamma-thionin-like	unknown protein, 8	gamma-zeathionin 1	gamma-purothionin	thionin precursor,
Π	T10243	T07917	T10183	T10823	T10176	T02622	F96787	T02621	G86328	S66221	S28991	S12246	S28989	866219	S28993	S28995	S28994	S66220	828990	866218	F96591	T14866	846272	T03673	857809	D96636	31	811529	23
DB	~														α												7		7
f Query Match Length	79	79	80	80	80	80	80	œ	S	20	30	161	27	4	25	27	56	54					152	89	105			47	105
Query Match	100.0	100.0	93.7	93.4	$\alpha$	92.7	91.0	90.4	55.5	53.8	50.2	48.2	47.2	46.7	45.8	45.5	45.2	44.7	44.5	•	38.7	38.7	35.0	33.7	27.4			25.1	
Score	301	301	282	281	279	279	274	272	167	162	151	145	142	140.5	138	137	136	134.5	~	129.5		116.5	105.5				77.5	75.5	75.5
Result No.	H	7	m	4	'n	9	7	æ	σ	10	11	12	13	14	15	16	17	18		20		22	23	24	25	26	27	28	29

gamma-thionin SI-a hordothionin gamma gamma-thionin SI-a gene serrate prote surface protein 51 neurotoxin III -s neurotoxin III -s proteinase inhibit defensin AMP2 - Da proteinase inhibit disease resistance defensin 1 precurs transforming growt disease resistance defensin precurs transforming growt disease resistance defensin precurs transforming growt disease resistance purothionin gamma neurotoxin XI - sc	radish ish) vision 16-Jul-1999 #text_change 20-Jun-2000 vision 16-Jul-1999 #text_change 20-Jun-2000 Penninckx, I.J.; Osborn, R.W.; Broekaert, W.F. ry, April 1996 d from GB/EMBL/DDBJ  Ronde Rode Kleine Witpunt  Ronde Rode Kleine Witpunt ein 3 #status predicted <sig> ein 3 #status predicted <mai></mai></sig>
S69146 S13846 S13844 S16144 S16144 T28669 NTSR3B NTSR3B D84482 S66222 T06667 T06667 T067897 T067897 S11530 NTSREB	Precursor - radish sations (radish) #sequence_revision 16-Jul-1999 deris, I.J.; Penninckx, I.J.; O L Data Library, April 1996 Z16994 y; translated from GB/EMBL/DDBJ R> EMBL:X97319 e: cultivar Ronde Rode Kleine W all sequence #status predicted <s #status="" 3="" <s="" all="" ifungal="" predicted="" predictions="" protein="" seq<="" sequence="" td=""></s>
86914 81344 81344 816148 81664 172866 172866 172866 17289 17289 17089 17089 17089 17089 17089 17089 17089	AL. dish) evishon evishon y Penni; ary, App ary, App Ronde ] Ronde ]
H N N N N N N H H N N N N N N	
4477 2203 2203 2333 2333 2333 2333 2333 23	SULT 1  0243  Ciffungal protein 3 precursor - rad Species: Raphanus sativus (radish) Date: 16-Jul-1999 #sequence_revish Accession: T10249  Fetrance to the EMBL Data Library, Accession: T10243  Status: prelliminary; translated fr Molecule type: MRNA Residues: 1-79 - KERA Cross-references: EMBL:X97319  Gene: AFP3  Gene: AFP4  Gene: AFF4  Gene
8886448448	3 pp # sa pp #
4 4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6	protein Raphanus Jul-1999 : T10243 o. K.G. 26 o. the EM number: relimina relimina type: mR type: mR type: mR 1ype: mR 1ype: mR 1ype: mR 1ype: mR in: signm in: signm
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	rot alpha R.G R.G T11-7 T11-7 T11-7 T1-7 T1-7
444	1 P. S.
6 6 6 6 7 7 9 9 9 9 9 9 9 9 9 9 9 9 9 9	RESULT 1 T10243 antifungal protein 3 precursor C; Species: Raphanus sativus (rac C; Date: 16-Jul-1999 #sequence_r C; Accession: T10243 R; Terrax; F.R.G; Goderis, I.J: submitted to the EMBL Data Libr A; Reference number: 216994 A; Accession: T10243 A; Scatus: preliminary; translat A; Scatus: preliminary; translat A; Molecule type: mRNA A; Residues: 1-79 < TER>A; Cross-references: EMBL:X97319 C; Genetics: A; Genetics: A; Genetics: A; Gene: AFP3 C; Superfamily: gamma-thionin C; Keywords: antifungal pro

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THOUTON THE THE THEORY OF THE 
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
C;Accession: T02622; D84655;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, E.M.; Crosby, M.L.; Brandon, R.C.; Sykes, S;
R;Reference number: 214681
A;Reference number: 214681
A;Reference number: BMBL, ACO04747; NID: 33413696; PID: 93413711
A;Rolecule type: DNA
A;Residues: 1-60 < ROU-
A;Cross-references: EMBL.ACO04747; NID: 93413696; PID: 93413711
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
B;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.,
Buture 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID: 20083487; PMID: 10617197
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0
1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
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Best Local Similarity 92.00
Best Local 6; Conservative
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artifungal protein 2 precursor - radish
C;Species: Raphanus sativus (radish)
C;Species: Raphanus sativus (radish)
C;Accession: 10-10-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
C;Accession: T10023; B42642
R;Terras, F.R.; Eggermont, K.; Kovaleva, V.; Raikhel, N.V.; Osborn, R.W.; Kester, A.; Re Plant Coll 7, 568-573, 1995
A;Title: Small Cysteine-rich antifungal proteins from radish: their role in host defense A;Reference number: 216976
A;Accession: T10023
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: man,A
A;Residues: 1-80 <TER>
A;Cross-references: EMBL:U18556; NID:g609319; PID:g609320
A;Residues: 1-80 <TER>
A;Cross-reference number: A20042; H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.B.; Vanderleyden, A;Title: Analysis of two novel classes of plant antifungal proteins from radish (Raphanu A;Reference number: A42842; MUID:92348373; PMID:1639777
A;Accession: B42842
A;Status: preliminary
A;Molecule type: protein
A;Reperimental source: seed
A;Note: sequence extracted from NCBI backbone (NCBIP:109572)
C;Punction: AFP
C;Genetics: AFP
C;Genetic
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C;Species: Raphanus sativus (radish)
C;Date: 16-Jul.1999 #sequence_revision 16-Jul.1999 #text_change 20-Jun-2000
C;Accession: T10183
R;Terras, F:R; Goderis, I.J.; Penninckx, I.J.; Osborn, R.W.; Broekaert, W.F.
submitted to the EMBL Data Library, April 1996
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              30 KLCERSSGTWSGVCGNNNACKNOCIRLEGAQHGSCNYVFPAHKCICYFPC 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: T10183
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Gtatus: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Station: T60 < TERA
A,Cross-references: EMBL:X97318
A,Stationinal source: cultivar Ronde Rode Kleine Witpunt
C,Genetics:
A,Gene: AFP4
C,Superfamily: gamma-thionin
C,Keywords: antifungal
F,1-29/Domain: signal sequence #status predicted <&IG>F,1-29/Domain: signal protein 4 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
93.7%; Score 282; DB 2; Length 80;
Best Local Similarity 90.0%; Pred. No. 2.5e-23;
Matches 45; Conservative 3; Mismatches 2; Indels
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C,Superfamily: gamma-thionin
F)1-43/Domain: signal sequence #status predicted <SIG>
F)4-80/Product: antifungal protein 2 #status predicted <MAT>
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55.5%;
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A;Map position: 2
A;Introns: 22/1
C;Superfamily: gamma-thionin
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44; Conserv
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Best Local Simi
Matches 26;
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Matches 4
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C;Accession: F95787
R;Thologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.X.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Mature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Sakano, H.
A;Authors: Salzberg, S.L.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: As6141; MUID:21016719; PMID:11130712
A;Cession: F96787
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-80 <STO>
A;Cenetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 1
C;Superfamily: gamma-thionin
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Accession: T02611, E34655
R; Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitteed to the EMBL Data Library, August 1998
A; Reference number: 214681
A; Accession: T02621
A; Accession: T02621
A; Accession: T02621
A; Reference number: 214681
A; Reference number: 214681
A; Reference number: 214681
A; Reference number: 214681
A; Residues: L*80 cROD*
A; Residues: 1-80 cROD*
A; Raul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
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A;Accession: D84655
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-80 <STO>
A;Cross-references: GB:AE002093; NID:g3413711; PIDN:AAC31234.1; GSPDB:GN00139
C;Genetics:
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Species: Arabidopsis thaliana (mouse-ear cress)
Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
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                                                                                                                                                                                                                                                                                                                Score 279; DB 2; Length 80
Pred. No. 5.2e-23;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                   92.7%;
                                                                                                                                                                                                                                                                                                                                                                         45; Conservative
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A,Introns: 22/1
C,Superfamily: gamma-thionin
                                                                                                                                                                     A; Gene: At2g26010; T19L18.18
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Best Local Similarity
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Appothetical protein F14Pl.6 - Arabidopsis thaliana

(Special 1970)

(Special 2070)

(Special 
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vente: Nature 402, 761-768, 1999
A)Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84655
A;Status: preliminary
A;Molecule type: DNA
A;Rossidues: L80 <STO>
A;Rossidues: 
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N;Aleznate names: seed antifungal protein
C;Species: Dahlia merckii
C;Species: Dahlia merckii
C;Bacession: S66221
C;Accession: S66221
R;Osborn, R.W.; de Samblanx, G.W.; Thevissen, K.; Goderis, I.; Torrekens, S.; van Len
R;Osborn, R.W.; de Samblanx, G.W.; Thevissen, K.; Goderis, I.; Torrekens, S.; van Len
A;FEBS Lett. 369, 257-262, 1995
A;Ftle: Isolation and characterisation of plant defensins from seeds of Asteraceae,
A;Feference number: S66218; MUID:95354848; PMID:7628617
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Pred. No. 3.2e-11;
6; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 1-50 < OSB>
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A, Reference number: S28989; MUID:93138130; PMID:8422949

A,Accession: S28989 A,Molecule type: protein A,Residues: 1-27 <TER> C,Superfamily: gamma-thionin

0;

Gaps

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Query Match 53.8%; Score 162; DB 2; Length 50; Best Local Similarity 54.0%; Pred. No. 9.9e-11; Matches 27; Conservative 5; Mismatches 18; Indels

C; Keywords: antifungal

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RESULT 14

Sefels

defensin AMPI - Clitoria ternatea

NyAlternate names: seed antifungal protein

C;Species: Clitoria ternatea

R;Osborn, R.W.; de Samblanx, G.W.; Thevissen, K.; Goderis, I.; Torrekens, S.; van Leuven, R;Diation and characterisation of plant defensins from seeds of Asteraceae, Fabs A;Reference number: S66219

A;Recssion: S66219

A;Recssion: S66219

A;Residues: I-49 <OSBb

C;Keywords: antifungal
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C;Species: Sinapis alba (white mustard)
C;Deccession: $28993
R;Terras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, FEBS Lett. 316, 233-240, 1993
A;Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae A;Reference number: $28989; MUID:93138130; PMID:8422949
A;Accession: $28993
A;Accession: $28993
A;Accession: 528993
A;Accession: 228993
A;Accession: 228993
A;Accession: 228993
A;Accession: 228993
A;Accession: 528993
A;Accession: 
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م
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                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.7%; Score 140.5; DB 2; Length 49;
49.1%; Pred. No. 1.9e-08;
tive 5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.8%; Pred. No. 2.1e-08;
Matches 23; Conservative 0; Mismatches 1; Indels
Length 27;
47.2%; Score 142; DB 2; Length 27
96.0%; Pred. No. 8.2e-09;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                  1 KLCERSSGTWSGVCGNNNACKNQCI 25
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Best Local Similarity 49.19
Matches 26; Conservative
         Query Match
Best Local Similarity 96.03
Matches 24; Conservative
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C;Species: Helianthus annuus (common sunflower)
C;Date: 21.Nov-1993 #sequence_revision 26-May-1995 #text_change 15-Sep-2003
C;Accession: S12246
R;Domon, C.; Evrard, J.L.; Herdenberger, F.; Pillay, D.T.N.; Steinmetz, A.
Plant Mol. Biol. 15, 643-646, 1990
A;Title: Nucleotide sequence of two anther-specific CDNAs from sunflower (Helianthus ann A;Reference number: S12245; MUID:91338702; PMID:2102380
                                                                                                                                                                                                                                                                                                                                   antifungal protein 1 - rape (fragment)
C;Species: Brassica napus (rape)
C;Species: Brassica napus (rape)
C;Date: 25-F6-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
C;Accession: S28991; S28992
R;Terras, F.R.G; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, FRBS Lett. 316, 233-246, 1993
FRILLE: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae A;Reference number: S28989; MUID:93138130; PMID:8422949
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A,Molecule type: mRNA
A,Residudes: 1-161 < DOMA-
A,Cross-references: EMBL:X53375; NID:g18812; PIDN:CAA37455.1; PID:g18813
F;1-8/Domain: signal sequence (fragment) #status predicted <SIG-
F;9-161/Product: anther-specific protein SF18 #status predicted <NAT>
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                                                                        1 ELCEKASKTWSGNCGNTGHCDNQCKSWEGAAHGACHVRNGKHMCFCYFNC 50
              1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 50.2%; Score 151; DB 2; Length 30 Best Local Similarity 92.9%; Pred. No. 9.8e-10; Matches 26; Conservative 0; Mismatches 2; Indels
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셤

A, Molecule type: protein A, Residues: 1-23 <TE2> C, Superfamily: gamma-thionin

A; Molecule type: protein A; Residues: 1-30 <TER> A; Accession: \$28992

C.Species: Brassica rapa (turnip)
C.Species: 25-Feb-1994 #sequence\_revision 01-Dec-1995 #text\_change 09-Jun-2000
C.Date: 25-Feb-1994 #sequence\_revision 01-Dec-1995 #text\_change 09-Jun-2000
C.Accession: 528989
F.TERTSAS, F.R.W.; Vanderleyden, J.; Cammue, F.TERS Lett. 316, 233-240, 1993
A.Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae

antifungal protein 1 - turnip (fragment)

RESULT 13

homo sapien homo sapien pisum sativ

pisum sativ

triticum ae buthus occi hirudo medi

leiurus qui brachydanio vigna ungui

rattus norv

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   AFP3.

Brassica napus (Rape).

Bukarsica napus (Rape).

Bukarsica, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bormatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

Bornatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

Burosids II; Brassicales; Brassicaceae; Brassica.

NCBI_TAXID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Nachan;
Sobn U., Lee C.M., Lee M.H., Kim U.H.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
cations (By similarity).
-!- SUBCELLUMAR LOCATION: Secreted.
-!- SUBCELLUMAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00940; GAMMA_THIONIN; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
Sland defense; Fungicide; Signal; Multigene family.
SIGNAL 1 29 POTENTIAL.
CHAIN 30 CYSTEINE-RICH ANTIFUNGAL PROTEIN 3.
CHAIN
            Q01783 F
P22064 H
Q14766 H
Q01784 F
P20159 t
P01486 B
P28503 H
                                                                                                                                  P01481 1
Q90y54 b
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                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 3 precursor (AFP3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 301; DB 1; 100.0%; Pred. No. 5.4e-27;
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                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                  SCX5_LEIQU
JAG3_BRARE
THGC_VIGUN
PSD2 PEA
D230 PEA
LTBS HUMAN
LTBL HUMAN
DR39 PEA
THG2 WHEAT
SCXB BUTOC
ITHC HIRME
S213 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U59459; AAB03224.1; -...
PIR; T07917; T07917.
HSSP; P30231; LAVU.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR00814; Knot1.
Pfam; PF00304; Gamma-thionin; 1.
Probom; P0002594; Germa-thionin; 1.
SWART; SM00505; Knot1; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
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32 79
43 64
49 73
53 75
79 AA; 8555 MW;
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50; Conservative
                                                                                                                                                                                                                                                                                          STANDARD;
 SEQUENCE FROM N.A.
 AFP3 BRANA
Q39313;
70.5
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                                                                                                                                                                                                                                                             RESULT 1
   024331 raphanus sa
P30230 raphanus sa
P30231 sinapis alb
P30225 brassica na
080995 arabidopsis
P30224 arabidopsis
P30224 arabidopsis
09699 sinapis alb
080994 arabidopsis
096123 arabidopsis
020296 sinapis alb
P22357 helianthus
P30228 brassica ra
P30228 brassica na
024115 nicotiana p
P81571 spinacia ol
P815726 nicotiana t
C024158 corghum bic
P20125 sorghum bic
P20125 sorghum bic
P201325 elejurus ativ
P81925 pisum sativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 039313 brassica na
024332 raphanus sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arabidopsis
beta vulgar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 androctonus
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                                                                                                      May 11, 2004, 16:50:53; Search time 11 Seconds (without alignments) 236.683 Million cell updates/sec
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                                                                                                                                                                                                1 KLCERSSGTWSGVCGNNNAC.....OHGSCNYVFPAHKCICYFPC
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Q9blm4
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                            141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF2B SINAL
AF2B HELAN
AFP1 HELAN
AFP1 BEARA
AFP2 BRARA
AFP2 BRARA
AFP2 BRARA
DEF1 CAPAN
THG1 MICPA
DEF2 SPIOL
THG1 MIZE
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AFP3 RAPSA
AFP4 RAPSA
AFP2 RAPSA
AFP1 SINAL
AFP1 BRANA
AFP1 ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFP2_ARATH
AFP1_ARATH
AF2A_SINAL
AFP3_ARATH
AFP4_ARATH
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Maximum Match 100%
Listing first 45 summaries
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                                                                             - protein search, using sw model
                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 200000000
                                                                                                                                                                     US-10-006-252A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SwissProt_42:*
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161
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Maximum DB
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Gaps

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POTENTIAL
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PIR, T10183; T10183.
HSSP; P30231; 1AVJ.
INTERPRO; IPR008176; Gamma-thionin.
INTERPRO; IPR00364; Knotl.
Pfam; PP00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
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44 65
50 74
54 76
80 AA; 8873 MW;
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Best Local 8
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or send an ena.

SMED; X97319; CAA65984.,
PIR; T10243; T10243.
A HSSP; P30231; JAVJ.
A HSSP; P30231; JAVJ.
A HSSP; P30231; JAVJ.
A HSSP; P30231; JAVJ.
BR InterPro; JPR00364; Gamma-thionin.
DR PFEMN; P500364; Gamma-thionin; 1.
DR SMART; SM00505; Knocl.; 1.
DR SMART; SM00505; Knocl.; 1.
DR SMART; P500940; GawMa THIONIN; 1.
DR PROSITE; P500940; GawMa THIONIN; 1.
STORNAL 30 POTENTIAL.
THAIN 30 POTENTIAL.
THAIN 30 POTENTIAL.
THAIN 31 79 BY SIMILARITY.
BY SIMILARITY.

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A 101; DB 1; Length 79;
A 101; DB 1; Leng
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Raphanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Ronde Rode Kleine Witpunt, TISSUE=Seed;
Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cations (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
Locr-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 4 precursor (APP4).
                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Cysteine-rich antifungal protein 3 precursor (AFP3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 AA
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                                                                                                                            STANDARD;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Broekaert W.F.;
                                                                                                                            AFP3 RAPSA
024332;
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024331;
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Raphanus sativus (Radish)

AFP4 RAPSA
ID AFP4 RA
ID AFP4 RA
ID AFP4 RA
ID 16-0CT
DT 16-0CT
DT 28-FEB
DE CYSTEI
GN AFP4.

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Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Enassicales; Brassicaceae; Raphanus.
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MEDINE=5529355; PubMed=7780308;
Terrae F.R.G., Eggermont K., Kovaleva V., Raikhel N.V., Osborn R.W.,
Kester A., Rees S.B., Torrekens S., van Leuven F., Vanderleyden J.,
                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
Broekaert W.F.,
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: Possesses antifungal activity sensitive to inorganic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 282; DB 1; Length 80; Pred. No. 6.9e-25; Indels 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYSTEINE-RICH ANTIFUNGAL PRC PYRROLIDONE CARBOXYLIC ACID SIMILARITY).
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BY SIMILARITY.
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BY SIMILARITY.
B5667B6441818C9 CRC64;
                                                                                                                                                                                                                                                                                                                         cations (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 2 precursor (AFP2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWART; SMOC505; KnoT1: 1.

SWOSITE; PSO0940; GAMMA, THIONIN; 1.

Plant defense; Fungicide; Signal; Multigene family;

Pyrrolidone carboxylic acid.
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us-10-006-252a-10.rsp

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AFP1_BRANA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license@ispecific (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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01-OTT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annocation update)
28-FBB-2003 (Rel. 41, Last annocation update)
Sinapis alba (White mustard) (Brassica hirta).
Sinapis alba (White mustard) (Brassica hirta).
Sukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
NCBI_TAXID=3728;
                   "Small cysteine-rich antifungal proteins from radish: their role in host defense.";
Plant Cell 7:573-588(1995).
                                                                                                                                                                                                                                             Terras F.R.G., Schoofs H.M.E., de Bolle M.F.C., van Leuven F., Rees S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.; "Analysis of two novel classes of plant antifungal proteins from radish (Raphanus sativus L.) seeds."; J. Biol. Chem. 267:153109(1992).
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYSTEINE-RICH ANTIFUNGAL PROTEIN PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             746110D9A8CE6370 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00940; GAMMA THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 281; DB 1;
Pred. No. 8.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AA.
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MEDLINE=96433791; PubMed=8836771;
Neumann G.M., Condron R., Polya G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P30231, 1AVJ.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR00814; Knotl.
Prom: PF00004; Gamma-thionin; 1.
ProDom: P0002594; G Purchionin; 1.
SWART; SM00505; Knotl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                MEDLINE=92348373; PubMed=163977;
Cammue B.P.A., Broekaert W.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U18556; AAA69540.1; -. PIR, T10823; T10823. HSSP; P30231; 1AYJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 93.4%;
1 Similarity 92.0%;
46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8875 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 46; Conserv
                                                                                                                                                     SEQUENCE OF 30-65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 AA;
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AFP1_SINAL
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RRITH REPRESENTATION OF THE PROPERTY OF THE PR
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MEDIANE=98300344; PubMed=9636715;
Fant F., Vranken W.F., Broekaert W.F., Borremans F.A.M.;
"Determination of the three-dimensional solution structure of Raphanus
sativus antifungal protein 1 by 1H NVR.";
J. Mol. B101. 279:257-270(1998).
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica napus (Rape), and
Raphanus sativus (Radish).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids;
eurosids II; Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00505; Knotl; 1.

PROSITE; PS00940; GAMMA_THIONIN; 1.

Plant defense; Fungicide; 3D-structure; Pyrrolidone carboxylic acid.

MOD RES

DISULFID

4 51
                                                                                                                                                                                                                                            Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W., anderleyden J., Cammue B.P.A., Broekeert W.F.; "A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cations.
-!- SUBUNIT: Forms oligomers in its native state.
-!- MASS SPECTROMETRY: MW=5677; MW ERR=1.0; METHOD=Electrospray.
"Purification and mass spectrometry-based sequencing of yellow mustard (Sinapis alba L.) 6 kDa proteins. Identification as antifungal proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KLCERPSGTWSGVCGNNNACKNQCINLEKARHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 279; DB 1; Length 51;
Pred. No. 9.8e-25;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the plant defensin family
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P30225; Q41163;
10-AR-1993 (Rel. 25, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 1 precursor (AFP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           770990E72DD1C469 CRC64;
                                                                                            Int. J. Pept. Protein Res. 47:437-446(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB; 1AVJ; 28-JAN-98.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
                                                                                                                                                                                                                      MEDLINE=93138130; PubMed=8422949;
                                                                                                                                                                                                                                                                                                                                                                      FEBS Lett. 316:233-240(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 92.0
Matches 46; Conservative
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                                                                      antifungal proteins.
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                                                                                                                                                         SEQUENCE OF 1-25.
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SEQUENCE
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us-10-006-252a-10.rsp

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MEDLINE-20083487; PubMed=10617197;

MEDLINE-20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Lin X., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,

Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,

Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,

Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,

Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                               nianiuupsis Luainaua (mousereai Cless).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Probable cysteine-rich antifungal protein At2g26010 precursor (AFP).
AT2G26010 OR T19L18.18.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                eurosids II; Bran
NCBL TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
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                                                                                                                                                     SEQUENCE OF 30-73.
SEQUENCE OF 30-73.
SPECIES=31.03918; TISSUE=Seed;
MEDLINE=9318,0; PubMed=8422949;
Terras F.R.G. 1 Torrekens S., van Leuven F., Osborn R.W.,
Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
A new family of basic cysteine-rich plant antifungal proteins from
Brassicaceae species.";
FEBS Lett. 316:233-240(1993).
     Kester A., Rees S.B., Torrekens S., Van Leuven F., Vanderleyden J., Cammue B.P.A., Broekaert W.F.; "Small cysteine-rich antifungal proteins from radish: their role in
                                                                                                                                                                                                                                                                                                                                                                                                       SPECTES=R.sativus; IISSUE=Seed; MEDLINE=92348373; PubMed=163977; Farras F.R.G., Schoofs H.M.E., de Bolle M.F.C., van Leuven F., Terras F.R.G., Schoofs H.M.E., de Bolle M.F.C., van Leuven F., Races S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.; "Analysis of two novel classes of plant antifungal proteins from J. Seeds."; Seeds."; Seeds."; J. Bacal. Chem. 257:15310-15309(1992).
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYSTEINE-RICH ANTIFUNGAL PROTEIN 1.
PYRROLIDDOE CARBOXYLIC ACID.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
0SB90FAAC8DA6CZE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: Forms oligomers in its native state.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00940; GANN'A_THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family;
Pyrrolidone carboxylic acid.
1 29
SIGNAL 1
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InterPro; IPR008176; Gamma-thionin.
InterPro; IPR008614; Knorl.
Pfam, PF00304; Gamma-thionin, 1.
ProDom; PD002594; G Purochionin, 1.
SWART; SM00505; Knorl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U18557; AAA69541.1; -. PIR; T10176; T10176.
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8734 MW;
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Local Similarity 92.0%;
les 46; Conservative
                                                                                                         Plant Cell 7:568-573(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYSTEINE-RICH ANTIFUNGAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Nature 402:761-768(1999).
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic cations (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: Belongs to the plant defensin family.
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PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 KLCEKPSGTWSGVCGNSNACKNQCINLEGAKGGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 92.7%; Score 279; DB 1; Length 80; Best Local Similarity 90.0%; Pred. No. 1.5e-24; Matches 45; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
99EIBOD4443AD67B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probom; PRO02594; G Parothionin; 1.
SMART; SM0050594; G Parothionin; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
Prolidene; Fungicide; Signal; Multigene family; Pyrrolidene carboxylic acid. RV RTMITABITE 1.
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ID AFPI ARATH

STANDARD; PRT; 80 AA.

AC P302Z4; Q42179;

DT 01-APR-1998 (Rel. 25, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROBABLE
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InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                                                                                                                                                                                                                                                                                                        EMBL; AC004747; AAC31234.1; -. PIR; T02622; T02622.
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8580 MW;
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Gaps

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3; Indels

1; Mismatches

Best Loca Matches

8 셤

31 KLCERPSGTWSGVCGNNNACKNQCINLEKARHGSCNYVFPAHKCICYFPC 1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC

(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)

16-OCT-2001 16-OCT-2001 28-FEB-2003 AFP2 ARATH

AFP2 ARATH
ID AFP2 AF
AC 080995;
DT 16-OCTDT 16-OCTDT 28-FEB-

80 AA

STANDARD;

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RECORDING FROM N.A.

STRAIN=CV. Columbia.

RA Theologis A., Ecker J.R., Palm C.J., Pederspiel N.A., Kaul S.,

RA Theologis A., Ecker J.R., Palm C.J., Pederspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White D., Alonso J., Conway A.B., Chenk R.F., Chin C.W.,

RA Ching M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fulia C.Y.,

RA Gill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Hulzar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Langin-Hooper S., Lee A., Lee J.M., Larz C.A., Li J.H., Li Y.-P.,

RA Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Will, T. Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Voysotskaia V.S., Walker M.,

RY "Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
Cysteine-rich antifungal protein 1 precursor (AFP1) (Anther-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W., Vanderleyden J., Cammue B.P.A., Broekaert W.F.; An new family of basic cysteine-rich plant antifungal proteins from Brassicaceae species."

FEBS Lett. 316:233-240(1993).

-I- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99178804; PubMed=10080719;
Williams R.W., Clark S.E., Meyerowitz E.M.;
Genetic and physical characterization of a region of Arabidopsis chromosome 1 containing the CLAMATA1 gene.";
Plant Mol. Biol. 39:171-176(1999).
                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: Forms oligomers in its native state.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
                 SEQUENCE FROM N.A.
STRAIN=Cv. Columbia; TISSUE=Seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93138130; PubMed=8422949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z27258; CAA81770.1; -. EMBL; Z29957; CAA82845.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 30-56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thaliana.";
                                                                                                                                                                                                                                                                                                                                    Raynal M.
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 274; DB 1; Length 80; Pred. No. 5.3e-24; 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99F34A8DA360441F CRC64;
                                                                                                                                                                                                                                                                 ProDom; PD002594; G_Purothionin; 1.
SMART; SW00505; Knocl; 1.
PROSITE; PS00940; GAWMA_THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRROLIDONE CARB
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
C -> F (IN REF.
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                                                                                                                             HSSP, P30231, 1AYJ.
Incerror, PRROBATTG, Gamma-thionin.
Incerror, PROBAT4, Knot1.
Pfam, PP00304; Gamma-thionin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                            EMBL; AF049870; AAD02502.1; -. EMBL; AC007396; AAF26754.1; -. PIR; F96787; F96787.
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30
80
65
74
74
33
8709 MW;
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EMBL; X91916; CAA63009.1;
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P30232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD RES
DISULFID
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CONFLICT
SEQUENCE
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SINAL
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AF2A_SI
DR KWW KWW THE LEAR T
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Streptophyta, Embryophyta, Tracheophyta, eurosids II; Brassicales, Brassicaceae, Sinapis. 01-APR-1993 (Rel. 25, Created)
01-OTT-1996 (Rel. 34, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 2A (AFP2A) (MZA).
Sinapis alba (White mustard) (Brassica hirta). 

MEDLINE=96433791, PubMed=8836771; Neumann G.M., Condron R., Polya G.M.; "Purification and mass spectrometry-based sequencing of yellow mustard (Sinapis alba L.) 6 kDa proteins. Identification as TISSUE=Seed; SEQUENCE

Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W., Vanderleyden J., Cammue B.P.A., Broekaert W.F., Brannily of basic cysteine-rich plant antifungal proteins from Brassicaceae species."; FEBS Lett. 316:233-240(1993). Int. J. Pept. Protein Res. 47:437-446(1996). MEDLINE=93138130; PubMed=8422949; antifungal proteins."; SEQUENCE OF 1-26.

-!- FUNCTION: Possesses antifungal activity sensitive to inorganic cations.
-!- SUBDNIT: Forms oligomers in its native state.
-!- MASS SPECTROMETRY: WW=5705; MW ERR=0.8; METHOD=Electrospray.
-!- SIMILARITY: Belongs to the plant defensin family. HSSP, P30231; 1AYJ. InterPro; IPR008176; Gamma-thionin. InterPro; IPR003614; Knot1. Pfam; PF00304; Gamma-thionin; 1. ProDom; PD002594; G\_Purothionin; 1.

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                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                16-0CT-2001 [Rel. 40, Last sequence update)
Probable cysteine-rich antifungal protein At2g26020 precursor (AFP).
ATZG26020 OR T19I18.17
ATZGACO20 OR T19I18.17
Bukaryota, Viriallanae (Nouse-ear cress).
Bukaryota, Viriallanae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CV. Columbia, MEDLINE-20083487; PubMed=10617197; Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman M.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                  1 KLCERSSGIWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
                                                                                                                                                                                                                          2 KLCQRPSGTWSGVCGNNNACRNQCINLEKARHGSCNYVFPAHKCICYFPC 51
                                                                                                                                               Length 51;
  SMART; SMUGDUS, ALOLI, T.

PROSTIE; PROGDOSO; CAMAA_THIONIN; 1.

PROSTIE; PROSPORYLATION, PYINOIDOR CARDOXYLIC ACID.

MOD RES 1.

PHOSPHORYLATION (BY CDPK).

DISULID 15 36 BY SIMILARITY.

DISULRID 21 45 BY SIMILARITY.

DISULRID 25 47 BY SIMILARITY.

SKENIENCE 51 AA; 5722 MW; 1C7FSOE72DC945BI CRC64;
                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00940; GAMMA THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cations (By similarity).
SUBCELLULAR LOCATION: Secreted (By similarity)
                                                                                                                                             Score 273; DB 1;
Pred. No. 4.5e-24;
                                                                                                                                                                                                                                                                                              80 AA.
                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AC004747; AAC31244.1; -.
PIR; T02621; T02651.
BSSP; P30231; LAY.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00304; Gamma-thionin; 1.
                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
                                                                                                                                             90.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 402:761-768(1999).
SMART; SM00505; Knot1; 1.
                                                                                                                                                                           44; Conservative
                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00505; Knot1;
                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter J.C.;
                                                                                                                                                                                                                                                                                           AFP3_ARATH
080994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thaliana.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                              CYSTEINE-RICH ANTIFUNGAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-cv. Columbia, MEDLINE-99397451; PubMed=10470850; Kann B., Asamizu E., Kotani H., Kanbko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H., Miyajima N., Tabata S.; Structural analysis of Arabidopsis thaliana chromosome 5. IX. Sequence features of the regions of 1,011,550 bp covered by seventeen pland TAC clones."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
PROBABLE CYSTEINE-RICH ANTIFUNGAL PROTEIN
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QPF127; RSA7986;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Probable oysteine-rich antifungal protein LCR77 precursor (AFP).

Probable oysteine-rich antifungal protein LCR77 precursor (AFP).

Arabidopsis thaliana (Mouse-ear cress).

Arabidopsis thaliana (Mouse-ear cress).

Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vanoosthuyse V., Miege C., Dumas C., Cock J.M.;
Submitted (JUN-2000) to Swiss-Prot.
-!- FUNCIION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 KLCEKPSGTWSGVCGNSNACKNQCINLEGAKHGSCNYVFPAHKCICYVPC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
                                                                                PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                    Length 80;
                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                           SIMILARITY).
BY SIMILARITY.
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--- SUBCELLULAR LOCATION: Secreted (By similarity).
--- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00940; GAMMA THIONIN; 1.
Plant defense; Fungicidē; Signal; Multigene family;
Pyrrolidone carboxylic acid.
SIGNAL
1 29 POTENTIAL.
CHAIN 30 80 PROBABLE CYSTEINE-RICH
                                                                                                                                                                                                                                                                                                              Score 272; DB 1;
Pred. No. 8.8e-24;
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB017065; BAB09149.1; -.
HSSP; P30231, 1AXV.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Kncl.
Pfam; PF00304; Gamma-thionin; 1.
ProDom; P0002594; G Purchionin; 1.
SMART; SM00505; Kncl!; 1.
                                                                                                                                                                                                                                                                                                                 90.4%;
                                                                                                                                                                                                                                                         8640 MW;
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                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                   30
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DISULFID
SEQUENCE
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                                                                                      MOD_RES
                              CHAIN
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DISULFID DISULFID DISULFID

SEQUENCE Query Match

Best Loca Matches

DISULFID

FT FT FT FT SO SO

MOD\_RES

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

SEQUENCE TROM N.A.

Model STAIN-cv. HA401B / Cargill; TISSUE-Anther;

M EDALINE-3138702, PubMed-2102380;

A Domon C., Evrard J.-L., Herdenberger F., Pillay D.T.N., Steinmetz A.;

R (Helianthus annual L.)..;

Plant Mol. 3iol. 15:643-646(1990).

C -!- FUNCTION: Anther-specific cell wall protein which could contribute control and larchitecture of epidermal anther cells via intermolecular disulfide bridges.

C -:- TISSUE SPECIFICITY: Epidermal anther cells.

CC -:- DEVELOPMENTAL STAGE: Late developmental stages.

CC -:- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-mib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                 eudicots; asterids;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1999 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last amnotation update)
Anther-specific protein SP18 precursor (Fragment).
Helianthus annus (Common sunflower).
Eukaryota, Viridiplantee, Streptophyra, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; asterianganulids; Asterales, Asteraceae, Asteroideae, Heliantheae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR'1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 21, Last annotation update)
Cysteine-rich antifungal protein 1 (AFP1) (Fragment).
Brassica rapa (Turnip).
Brkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KLCERSSGTWSGVCGNNNACKNOCIRLEGAQHGSCNYVFPAHKCICYFPC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.2%; Score 145; DB 1; Length 161;
llarity 46.0%; Pred. No. 1.9e-09;
Conservative 8; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTHER-SPECIFIC PROTEIN SF18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAMMA-THIONIN LIKE DOMAIN. PROLINE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27A9CF4633ADA02B CRC64;
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SIMILARITY.
SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR, S12246; S12246.
HSSP, P30231; LAVJ.
Interbro; IRR08116; Gamma-thionin.
Interbro; IRR08116; Knot1.
Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
Signal; Cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY
BY
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161
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                                                                                                                                                                  NCBI_TaxID=4232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Focal S. ... 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFP1_BRARA
AC P3027;
DT 01-APR-1993
DT 01-FEB-1994
DT 28-FEB-2003
DE Cysteine-ric
OS Brassica rapp
OC Eukaryota; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
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NON TER
SIGNAL
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Matches
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                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Sinapis alba (White mustard) (Brassica hirta).
Sinapis alba (Wridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
NCBI_TAXID=3728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYRROLIDONE CARBOXYLIC ACID (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Int. J. Pept. Protein Res. 47.437-446(1996).
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Forms oligomers in its native state.
-!- MASS SPECTROWETRY: MW=5840; MW_ERR=1.2; METHOD=Electrospray.
-!- SIMILARITY: Belongs to the plant defensin family.
HSSP; P30231; JAYJ.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR008176; Knot1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
         PYRROLLDONE CARBOXYLIC ACID (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
2D0DAFB38E3BE321 CRC64;
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                                                                                                                                                                                                                           1 KLCERSSGTWSGVCGNNNACKNOCIRLEGAQHGSCNYVFPAHKCICYFPC 50
                                                                                                                                                                                                                                                MEDLINE=96433791, PubMed=8836771, Neumann G.M., Condron R., Polya G.M., "Purification and mass spectrometry-based sequencing of yellow mustard (Sinapis alba L.) 6 kDa proteins. Identification as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLCERSSGTW-SGVCGNNNACKNOCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 211.5; DB 1; Length 52;
Pred. No. 2.9e-17;
5; Mismatches 8; Indels
                                                                                                                                                               Length 80;
                                                                                                                                                       Score 272; DB 1; Length 80
Pred. No. 8.8e-24;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A060FCBC13A8D1FB CRC64;
                                                                                                                                                                                                                                                                                                                                                            52 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE, PS00940, GAMMA_THIONIN, FALSE Fungicide, Pyrrolidone carboxylic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD002594; G Purothionin; 1. SMART; SM00505; Knot1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00304; Gamma-thionin; 1.
                                                                                                                                                         90.4%;
                                                                                                                     8518 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5856 MW;
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les 44; Conservative
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                                                                                                                     80 AA;
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TISSUE=Seed;

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RESULT 12 AF2B SINAL

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MOD\_RES DISULFID

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Matches

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Gaps

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RESULT 13 ASF1\_HELAN ID ASF1\_HELAN AC P22357;

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Nanderleyden J., Cammue B.P.A., Brockeart W.F.;

M. Vanderleyden J., Cammue B.P.A., Brockeart W.F.;

"A new family of basic cysteine-rich plant antifungal proteins from
Brassicacae species.";

"EBS Lett. 316;233-240(1993).

-!- FUNCTION: Possesses some antifungal activity sensitive to
inorganic cations and antibacterial activity against B.megaterium.

-!- FUNCTION: Possesses some antifungal activity against B.megaterium.

-!- SIMILARITY: Belongs to the plant defensin family.

PIR, 528990; 528990.

PIR, 528990; 528990.

RIMSP, PANCAIT: Belongs to the plant defensin family.

PIRSP, PANCAIT: PROBB176; Gamma-thionin.

Probom, PD002594; G_Purcthionin. 1.

PROSTIE; PS00940; GAMMA THIONIN; 1.

PROSTIE; PS00940; GAMMA THIONIN; 1.

PROSTIE; PS00940; GAMMA THIONIN; 1.

MOD_RES | Implication Antibiotic; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps,
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01-APR-1993 (Rel. 28, Last sequence update)
01-EBB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 2 (AFP2) (Fragment).
Brassica rapa (Turnip).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales, Brassicaceae; Brassica.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=51350;
                                                                                                                                                                                         TISSUE=Seed;
MEDLINE=39138130; PubMed=8422949;
MEDLINE=39138130; PubMed=8422949;
Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
Vanderleyden J., Cammue B.P.A., Broekeart W.F.;
"A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae species.";
Passicaceae pecies.";
PEBS Lett. 316:233-240(11993).
-1- FUNCTION: Possesses antifungal activity sensitive to inorganic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBUNIT: Forms oligomers in its native state.
-1- SUBUNIT: Belongs to the plant defensin family.
PIR; S28999; S28989.
HSSP: P30231; 1ANJ.
InterPro; IPR008176; Gamma-thionin.
ProDom; PD002594; Gamma-thionin; 1.
PROSTIE; P800940; GAMMA_THIONIN; 1.
PROSTIE; P800940; GAMMA_THIONIN; 1.
Plant defense; Fungicide; Pyrrolidome carboxylic acid.
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 47.2%; Score 142; DB 1; Length 27
Best Local Similarity 96.0%; Pred. No. 7.6e-10;
Matches 24; Conservative 0; Mismatches 1; Indels
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27 AA; 2891 MW; 571E6D9C611D4A9E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KLCERPSGTWSGVCGNNNACKNQCI 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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MEDLINE=93138130; PubMed=8422949;
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SEQUENCE
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AFP2_BRARA
AFP2_BRARA
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      Query Match
      44.5%; Score 134; DB 1; Length 27;

      Best Local Similarity 92.3%; Pred. No. 5.8e-09;

      Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

      Qy

      I KLCERSSGTWSGVCGNNNACKNQCIR 26

      Db

      2 KLCERPSGTXSGVCGNNNACKNQCIR 27

      Search completed: May 11, 2004, 16:57:18

      Job time: 39 secs
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May 11, 2004, 16:53:44; Search time 39 Seconds (without alignments) 404.511 Million cell updates/sec
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301
1 KLGERSSGTWSGVCGNNNAC.....QHGSCNYVFPAHKCICYFPC 50
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Q94in7 brassica ol	Q8h6k0 brassica ra	Q9fs38 eutrema was	Q9fi22 arabidopsis	Q9fwr6 arabidopsis	Q8vzq7 arabidopsis	Q81sm8 helianthus	Q84zx5 artemisia v	Q9fz31 arabidopsis	Q40779 picea abies	Q8gtl2 picea abies	Q40539 nicotiana t	P82788 arabidopsis	P82789 arabidopsis	Q40128 lycopersico	Q948t2 pyrus pyrif
SUMMARIES		QI	Q94IN7	OSH6K0	Q9FS38	Q9F122	Q9FWR6	1 Q8VZQ7	Q8LSM8	_	Q9FZ31	040779	Q8GTL2	040539	P82788	P82789	040128	0948T2
		ngth DB	80 10	80 10	80 10	80. 10	56 10	78 10	•	132 10	80. 10	83 10	83 10	83 10	77 10	108 10	105 10	81 10
	ouerv	Match Length DB	94.4	94.0	92.7	90.4	55.5	55.5	51.2	42.9	38.7	38.7	38.4	33.7	28.7	27.7	27.4	27.1
		Score	284	283	279	272	167	167	154	129	116.5	116.5	115.5	101.5	86.5	83.5	82.5	81.5
	Result	No.	Н	7	М	4	ហ	9	7	æ	σ	10	11	12	13	14	15	16

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Gaps

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Query Match 94.4%; Score 284; DB 10; Length 80; Best Local Similarity 94.0%; Pred. No. 1e-29; Matches 47; Conservative 1; Mismatches 2; Indels

31 KLCERPSGTWSGVCGNNNACKNQCIRLEKARHGSCNYVFPAHKCICYFPC 80 1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC

DP. 8

Q948t3 pyrus pyrif Q948t4 pyrus pyrif Q9410s nicotiana e Q90247 arabidopsis Q81996 arabidopsis Q81996 arabidopsis Q81996 arabidopsis Q81996 arabidopsis Q81406 nicotiana a Q80406 apsicum an Q81410 perunia hyb Q81490 Uyrechinus Q91091 androctonus Q91091 arabidopsis Q91411 paramecium Q92011 arabidopsis Q9111 paramecium Q92011 arabidopsis	V72169 lampetra ja Q72169 lampetra ja Q8h766 elaeis guin Q8h66 elaeis guin Q24225 oryza sativ Q9fr81 pisum sativ Q8lgd4 arabidopsis Q8lgd4 arabidopsis Q8l698 triticum ae	odate) update)	Embryophyta; Tracheophyta; edons; core eudicots; rosids; Brassica.	n."; k/DDBJ databases. ein activity; IEA. 8D2690 CRC64;
		<b>4</b> 5 5	Embry dons; Brass	'"; /DDBJ in ac 102690
	MENT	ed) sequence un annotation	ta; tyle; ae;	o ani Dr.
Q948T3 Q948T4 Q948T4 Q9C241 Q9C347 Q8CEGG Q8C Q8CEG Q8CEG Q8C Q8C Q8C Q8C Q8C Q	072769 084766 084766 024225 09FR81 09FR81 08LGD4 08SBH3 08L698	PRT; Created) Last seq Last ann	er). reptophy ; eudico assicace	gene for defensin."; the EMBL/GenBank/DDBJ 8.1;se/immunity protein act mma-thionin. otl: ionin; 1. iothionin; 1tHIONIN; 1THIONIN; 1THIONIN; 1THIONIN; 1THIONIN; 1THIONIN; 1THIONIN; 1.
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C20202020202020202020202020202020202020	7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		oleracea; viridi hyta; Ma II; Bras D=3712;	R.; ad olerace ad (APR-20 3311046; C 3311046; C 3003793; F 37 IPRO036 37 IPRO036 37 IPRO036 38 IPRO05059; E 38 IPRO06051 3
88 8811:5	7 117 100 100 100 100 100 100 100 100 10	T 1 W7 W7 W94IN7 W94IN7; 01-DEC-2001 01-OCT-2003 Defensin pre	Brassica oleracea (Cauliflower). Bukaryota, Viridiplantae; Streptophyta; Embr. Spermatophyta; Magnoliophyta; eudicotyledons eurosids II; Brassicales; Brassicaceae; Brass NCBI_TaxID=3712; SEQUENCE FROM N.A.	Esnault R.;  Brassica oleracea def gene for defen Submitted (APR-2001) to the EMBL/GenB EMBL; AJ311046; CAC37558.1; GO; GO:0003793; F:defense/immunity pr InterPro; IPR008176; Gamma-thionin. InterPro; IPR003614; Knotl. Probom; PP002594; Gpurothionin; 1. SYMART; SM00505; Knotl; 1. SYMART; SN00505; Knotl; 1. Signal. SiGNAL. SEQUENCE 80 AA; 8740 MW; 980477DF
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92.7%; Score 279; DB 10;
88.0%; Pred. No. 4.6e-29;
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                                                                                                                                                                                                                                                                             (TrEMBLrel. 16,
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                                            Conservative
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Best Local Similarity
Matches 44; Conserv
                        Similarity
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01-OCT-2003 (TrEM
F14P1.6 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Columbia;
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01-MAR-2001
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      Query Match
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Matches 4
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Q9FWR6
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XX MEDLINE=21071227; PubMed=11204773;

XX Saitch H., Kiba A., Nishihara M., Yamamura S., Suzuki K., Terauchi R.;

Xaitch H., Kiba A., Nishihara M., Yamamura S., Suzuki K., Terauchi R.;

Xaitch H., Kiba A., Nishihara M., Yamamura S., Suzuki K., Terauchi R.;

Xi Saitch H., Kiba A., Nishihara M., Yamamura S., Suzuki K., Terauchi R.;

Yatch Virus X vector.";

Mol. Plant Microbe Interact. 14:111-115(2001).

R MBL, ABO12871; BAB19054.1; -.

R MSSP; P30212; IAVV.

GO: GO:0003793; F:defense/immunity protein activity; IEA.

R InterPro; IPR00314; Knotl.

R Pfam; P700314; Knotl.

R Pfam; P700314; Gamma-thionin; 1.

R Propon; P0002594; Gamma-thionin; 1.
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                                                                                                                                                                  Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage). Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                               Ryang S.-H., Chung S.-Y., Park Y.-S., Cho T.-J.,

"Characterization of Chinese cabbage genes induced by Pseudomonas syringae pv. tomato.";

Syringae pv. tomato.";

Submitted (JUL_2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF528180; AAN23105.1;

EMBL, AF528180; AAN23105.1;

InterPro; IPR00176; Gamma-thionin.

InterPro; IPR00364; Knot1.

Ppfam, PF00304; Gamma-thionin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probon, P0002594, G_Purothionin, 1.
PROBITE, BW0505, Knotl, 1.
PROSITE, PS00940, GAMMA THIONIN, 1.
SEQUENCE 80 AA, 8864 WW, 485CC5A95905E92C CRC64;
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POTENTIAL.
CF2F10ADD38FC87A CRC64;
                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                 80 AA.
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PROSITE; PS00940; GAMMA_THIONIN; 1.
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Bust Local Similarity 92.0%,
Trhes 46; Conservative
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                                                   PRELIMINARY;
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                                                         Gaps
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Makaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta; Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids.eurosids II; Brassicales, Brassicaceae; Arabidopsis.
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Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A.,
Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
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                                                                                                                                                           31 KLCEKSSGTWSGVCGNNNACKNQCINLEGARHGSCNYIFPYHRCICYFPC 80
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EMBL; AB017065; BAB09150.1; -
HSSP; B90231; IAVJ.
CO; GO:0003793; F:defense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR00304; Gamma-thionin.
ProDom; PF00304; Gamma-thionin; 1.
ProDom; PF0055; Knocli, 1.
SRART; SR00505; Knocli, 1.
PROSITE; SS00940; GAMMA_THIONIN; 1.
SEQUENCE 80 AA; 8550 MW; 44EIF6D8452AC76E CRC64;
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                                                                                                                  1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
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Length
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Last annotation update)
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Arabidopsis thaliana (Mouse-ear cress).
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Pfam; PF00304; Gamma-thionin; 1.
SMART; SM00505; Knot1; 1.
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Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Deng J.M., Goldsmith A.D., Lee J.M., Onodeza C.S., Quach H.L.,
Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
Theologis A.;
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Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
55.5%; Score 167; DB 10; Length 78;
Best Local Similarity 52.0%; Pred. No. 2.2e-14;
Matches 26; Conservative 6; Mismatches 18; Indels
                                                                                                                                                                                        GO, GO:0003793; F:defense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Indels
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MART; SM00505; Knoč1, 1.
PROSITE; PS00940; GAMA THIONIN; 1.
SEQUENCE 56 AA; 6403 WW; 3BD56EAA25EBC442 CRC64;
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; 8840 MW; A5B5DD28303A6545 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBVZQ7;
QBVZQ7;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative defensin AMPI protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 167; DB 10;
Pred. No. 1.6e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                      Pfam; PF00304; Gamma-thionin; 1
                                                                                          EMBL; AC024609; AAF98402.1; -. PIR; G86328; G86328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 55.5%;
l Similarity 52.0%;
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
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Q8VZQ7
      SORRERE
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae, Asteroideae; Heliantheae;
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Eukaryota, Vitidiphantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Asteroideae; Anthemideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Himly M., Jahn-Schmid B., Dedic A., Kelemen P., Wopfner N., Altmann F., van Ree R., Briza P., Richter K., Ebner C., Ferreira F.; "Art v 1, the major allergen of mugwort pollen, is a modular glycoprotein with a defensin-like and a hydroxyproline-rich domain."; FASEB J. 17:106-108(2003).
BMBL, AR493943, AAO24900.1; -.
GO; GO:0003793, F:defense/immunity protein activity; IEA.
InterPro; IPR0081614; Knot1.
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20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hu X., Bidney D., Duvick J., Yalpani N., Crasta O., Folkerts
Lu G.;
1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 108;
                              1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF364865, AAM77914.1;
GO, GO:0003793; F:defense/immunity protein activity; IEA.
InterPro; IPR00816; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002584; G Purchionin; 1.
SMART; SW0505; KnoEl; 1.
SEQUENCE 108 AA; 11866 MW, 631ECD8F02F21AD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CGT-2003 (TrEMBLrel. 25, Last annotation update)
Major pollen allergen Art v 1 precursor.
                                                                                                                                                                                                                                                                                    01-0CT-2002 (TrEMBLrel. 22, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Oxalate oxidase confers Sclerotinia resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 154; DB 10;
Pred. No. 1.5e-12;
6; Mismatches 19;
                                                                                                                                                                                                    108 AA.
                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                             Helianthus annuus (Common sunflower)
                                                                                                                                                                                                    PRT;
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MEDLINE=22409970; PubMed=12475905;
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Best Local Similarity 50.00,
                                                                                                                                                                                                 PRELIMINARY;
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SEQUENCE
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Q40779
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Matches
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MEDLINE=21016719; PubMed=11130712;
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Duchler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn. L., Conway A.B., Conway A.R., Comyay A.R., Forng B., Fuli C.Y.,
Chung M.K., Conn. L., Conway A.B., Forng B., Fuli C.Y.,
Chung M.K., Conn. L., Conway A.B., Forng B., Fuli C.Y.,
Chung M.K., Conn. L., Conway A.B., Kang J.-D., Forng B., Fuli C.Y.,
Chung M.K., Conn. L., Conway A.B., Kansen B., Huizar L.,
Chung M.K., Conn. L., Conway B., Hansen N.F., Hughes B., Huizar L.,
Chung M.K., Conn. C., Khan A., Khaykin B.,
Lin C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Liam B.,
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
Militecher J., Miranda M., Nguyen M., Nicaman W.C., Osborne B.I.,
Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Change C. M., Vaysberg M., Wysotskaia V.S., Walker M.,
Mu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                            1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHK------CICYFPC 50
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A.,
Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (AuG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative antifungal protein (Cysteine-rich antifungal protein,
                                                                                                                             Length 132;
                    POTENTIAL.
MAJOR POLLEN ALLERGEN ART V 1.
745249C89919F316 CRC64;
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GO; GO:0003793; F:defense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knoctl.
                                                                                                                                                                                    11; Indels
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                                                                                                                          ch 42.9%; Score 129; DB 10; Similarity 45.6%; Pred. No. 3.6e-09; 26; Conservative 6; Mismatches 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                         80 AA.
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ProDom; PD002594; G_Purothionin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                       1 24 PC
25 132 MJ
132 AA; 13404 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 408:816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F24C10.12 OR F14C21.57.
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                                                                                                                                Query Match
Best Local S
Matches 26
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                                                                              SEQUENCE
Signal
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after seed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sharma P., Linneborg A., Isolation of a cDNA encoding a gamma-thionin-isolation and characterization of a comma-thionin-like protein from roots of Norway spruce.", Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 25, Last sequence update)
01-Cr7-2003 (TrEMBLrel. 25, Last sequence update)
putative plant defensin SPI1B.
putative plant defensin SPI1B.
Picca abies (Norway spruce) (Picca excelsa)
Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 picea abies (Norway spruce) (Picea excelsa).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
NCBI_TaxID=3329;
                                                                                                                                                              1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHK-CICYFPC 50
                                                                                                                                                                                                                       30 ELCKRESETWSGRCVNDYQCRDHCINNDRGNDGYCAGGYPWYRSCPCFFSC 80
                                                                                        ۲;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 116.5; DB 10; Length 83; Pred. No. 9.9e-08; B; Mismatches 20; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The purative gymnosperm plant defensin (SPII) accumulates agermination and a related SPIIB cDNA is found in needles."; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                   20; Indels
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PIR; T14866; T14866.

HSSP; P41964; IMYN.

GO; GO:0003793; F:defense/immunity protein activity; IEA.

Interpro; IPR008176; Gamma-thionin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 32 POTENTIAL.
83 AA; 8835 MW; B94207ADAB8FE4AS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
    DB 10;
38.7%; Score 116.5; DB 1.
39.2%; Pred. No. 9.6e-08;
tive 10; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00104; Gamma-thionin; 1.
ProDom; PD002594; G Purothionin; 1.
SMART; SM00505; Knotl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00940; GAMMA_THIONIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 38.7%;
1 Similarity 42.0%;
21, Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
             Query Match
Best Local Similarity
Matches 20; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Root;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Con NCBI_TaxID=3329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rissum=Needle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fossdal C.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC OOC OOK SEL REPRESENTED THE PROPERTY OF THE
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IDENTIFICATION.
PubMed=11437247;
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[1]
SEQUENCE 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
P82789
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  A PAC OCCOOR SERVING THE SERVING SERVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicotiana tabacum (Common tobacco).
Bukaryota, Vitidiphantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnaliophyta; eudicotyledons; core eudicots; asterids;
Ismiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                              Gaps
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, rosids;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ezaki B., Yamamoto Y., Matsumoto H.; "Cloning and sequencing of the cDNAs induced by aluminium treatment and Pi starvation in cultured tobacco cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 KLCRRKSKTFSGYCFISEHCDEECKEKEGAKRGMCIKKSIFRRY-CYCYHKC 82
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                                                                                                                                                                                                                                                                                                                                              34 RICKTPSGKFKGVCASRNNCKNVC-QTEGFPSGSCDFHVANRKCYCSKPC 82
                                                                                                                                                                                                                                                                                                                1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
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                                                                                                                                                                                                            DB 10; Length 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 33.7%; Score 101.5; DB 10; Length Similarity 40.4%; Pred. No. 9.2e-06; 21; Conservative 6; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P30231; 1AYJ.

GO; GO:0003793; F:defense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G-Purothionin; 1.
                                                                                                                                                                                                                                                              21; Indels
                                                                                                   SMART; SM00505; Knočl; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
SEQUENCE 83 AA; 8888 WW; E45BF9E61B9AA3D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IIN; 1.
64780A4984E371B0 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein LCR79 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                          Score 115.5; DB 1
Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 AA
                                                                                                                                                                                                       Query Match
38.4%; Score 115.5;
Best Local Similarity 42.0%; Pred. No. 1.3e
Matches 21; Conservative 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                        InterPro; IPR003614; Knot1.
Pfam; PP00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
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WEBL; D29679; BAA0649.1; -.
PIR; T03673; T03673.
HSSP; P30231; 1AYJ.
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InterPro; IPR008176; Gamma-thionin
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Samsun;
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Best Local S
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Matches
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P82788
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5,
                           STRAIN=CV. Columbia, Membel=10617197, MEDLINE=20083487, Pubmed=10617197, Ed. R. Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buelli C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.Y., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., Vanaken S.B., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzboarg S.L., Fraser C.M., Venter J.C.; Salzboarg S.L., Fraser C.M., Venter J.C.; Squence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence features of the regions of 1,381,565 bp covered by twenty one physically assigned P1 and TAC clones.";
DNA Res. 5:131-145(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vancosthuyee V., Miege C., Dumas C., Cock J.M.;

"Two large Arabidopsis thaliana gene families are homologous to the
"Two large Arabidopsis thaliana gene families are homologous to the
Brassica gene superfamily that encodes pollen cost proteins and the
male component of the self-incompatibility response.";

In the Mol. biol. 46:17-34(2001).

EMBL; ACO06223; -; NOT ANNOTATED CDS.
InterPro; IPRO08175; Gamma-thionin.

R Pfam, PF00304; Gamma-thionin, 1.

ProDom; PD002594; G Purothionin; 1.

ProDom; PD002594; G Purothionin; 1.

ProDom; PD002594; G Purothionin; 1.

ProDom; PS00940; GAMMA_THIONIN; FALSE_NEG.

Hypothetical protein; Signal; Plant defense.
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STRAIN=cv. Columbia;
MEDLINE=98344145; PubMed=9679202;
Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
97194D61E5620DBE CRC64;
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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38.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 38.0 les 19; Conservative
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77
72
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FROM N.A.
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28
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77 AA;
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Divopersion esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Solanales; Solanaceae; Solanum.

NCBI_TaxID=4081;

NCBI_TaxID=
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Vanoosthuyse V., Miege C., Dumas C., Cock J.M.;
"Two large Arabidopsis thallana gene families are homologous to the brassica gene superfamily that encodes pollen coat proteins and that component of the self-incompatibility response.";
Plant Mol. Biol. 46:17-34(2001).
Plant Mol. Biol. 46:17-34(2001).
GO, GO:00003793; F:defense/immunity protein activity; IEA.
GO, GO:0003793; F:defense/immunity protein activity; IEA.
Hypothetical protein; Signal.
SIGNAL
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Flower-specific gamma-thionin-like protein/acidic protein
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CHAIN 23 108 HYPOTHETICAL PROTEIN LCR80.
SEQUENCE 108 AA; 11551 MW; 11E28E2CCE3578A7 CRC64;
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1 KLCERSSGTWSGVCGNNNAC.....QHGSCNYVFPAHKCICYFPC 50
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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## SUMMARIES

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Erassica napus (rape)

Brassica napus

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Cosids; eurosids II; Brassicales; Brassicacea; Brassica.

ICE 1 (bases 1 to 451)

RS Sohn, U., Lee, C.M., Lee, M.H. and Kim, J.H.

Brassica napus cDNAs

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Unpublished

OCE 2 (bases 1 to 451)

Exassica napus cDNAs

NCE 2 (bases 1 to 451)

Exassica napus cDNAs

NCE 2 (bases 1 to 451)

Exassica napus cDNAs

NCE 2 (bases 1 to 451)

Exassica napus cDNAs

NCE 2 (bases 1 to 451)

Example of Natrional University, Puk-Ku, Sankyuk-Dong 1370, Taegu

702-701, Korea

Track Sumission

Nobel 1 1 1996 this sequence version replaced gi:1293377.
         PLN 29-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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X97319.1 G1:1655684
XPP: antifungal protein 3.
Raphanus sativus (radish)
Raphanus sativus (radish)
Raphanus sativus
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
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   BNU59459

Brassica napus antifungal protein mRNA, complete cds.
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Terras, F.R.G., Goderis, I.J., Penninckx, I.J., Osborn, R.W. and Brockaert, W.F.
Unpublished
Unpublished
(Dases 1 to 475)
Terras, F.R.G.
Direct Submission
Submitted (O9-APR-1996) F.R.G. Terras, Institut fur
Submitted (O9-APR-1996) F.R.G. Terras, Institut fur
Halle (Saale), D-06120, FRG
Location/Qualifiers
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Characterization of Chinese cabbage genes induced by Pseudomonas syringae pv. tomato
Umbublished
2 (bases 1 to 363)
Park, Y.-S., Chung, S.-Y. and Cho, T.-J.
Direct Submission
Submisted (10-ULD-2002) Division of Life Sciences, Chungbuk
National University, Gae-Shin-Dong San 48, Cheongju 360-763, Korea
                                                              Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
roside; euroside II; Brassicales; Brassicaceae; Brassica.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Raphanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 AAGTTGTGCGAGAGGTCTAGTGGGACATGGTCAGGAGTATGTGGAAATAACAATGCTTGC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 LysAsnGlnCyslleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
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Broekaert,W.F.
Unpublished
   Brassica rapa subsp. pekinensis defensin mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                 22. 264
/note="induced by Pseudomonas syringae pv. tomato"
                                                                                                                                                                                                                                                                                                                                                               organism="Brassica rapa subsp. pekinensis"
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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AFP; antifingal protein 4.
Raphanus sativus (radish)
Raphanus sativus
                    AF528180
AF528180.1 GI:23321204
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Score:
Score:
Percent Similarity:
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/db_xref="GOA:Q91714"
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SONTACKNQCIRLERARHGSCNYVPPAHKCICXFPC"
/gene="def" 528. .550)
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Submitted (24-APR-2001) Esnault R., Institut des Sciences
Vegetales, C.N.R.S., Avenue de la Terrasse, 91 198 Gif sur Yvette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
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Indels:
Brassica oleracea def gene for defensin
Unpublished
2 (bases 1 to 933)
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                                                                                                                                                                  /organism="Brassica oleracea"
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|gene="def"
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/gene="def"
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product="defensin"
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/gene="def"
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284.00
96.00%
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824. .829
/gene="def"
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'gene="def"
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/gene="def"
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/gene="def"
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/gene="def"
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Unknown.
Unclassified.
1 (bases 1 to 285)
Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
Antifungal polypeptide and methods for controlling plant pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 05-DEC-1998
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                                                 'n
       Terras, F.R.G.
Direct Submission
Submitted (09-ARR-1996) F.R.G. Terras, Institut fur
Pflanzenbloothemie, Stress- und Entwicklungsbiologie, Weinberg
Halle (Saale), D-06120, FRG
Location/Qualifiers
                                                                              1. .499
//organism="Raphanus sativus"
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//oultivar="Ronde Rode Kleine Witpunt"
/db_xref="taxon:3726"
/dex Raage="adult plants infected with Alternaria brassicola"
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Matches:
Conservative:
Mismatches:
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/gene="AFP"
/gene="AFP"
/gene="AFP"
/product="antifungal protein 4"
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Sequence 17 from patent US 5773696.
AR014693.1 GI:3972147
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Location/Qualifiers
1. 285
/organism="unknown"
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44. .286
/gene="AFP"
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AR014693
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/mol\_type="unassigned DNA"

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PAT 18-DEC-2003
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Liang.J., Shah.D.M., Wu.Y.S. and Rosenberger,C.A.
Antifungal polypeptide AlyAFP from Alyssum and methods controlling plant pathogenic fungi
Patent: US 6653280-A 17 25-NOV-2003;
Location/Qualifiers
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Sequence 17 from patent US 6653280.
AR432393 AR432393.1 GI:40194670
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Seguence 41 from Patent WO9416076.
A39553
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                                                                                   (1-285)
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Alignment Scores:
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                  unidentified
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Dubock, A.C., Powell, K.A. and Rees, S.B.
ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
Parent: WO 9416076-A 41 21-JUL-1994;
ZENECA LTD (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.
(I (bases I to 288)
Broekaert, W. E., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Blocidal proteins
Patent: US 5824669-A 58 20-OCT-1998;
Location/Qualifiers
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Mismatches:
Indels:
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Location/Qualifiers
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Sequence 58 from patent US 5824869.
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                                                           133 AAGTTGTGCCAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 192
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Broekeert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: Us 5538525. 58 23-JUL-1996;
Location/Qualifiers
1. 288
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Brockaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: Use 6187304-A 58 13-FEB-2001;
Location/Qualifiers
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Matches:
Conservative:
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Sequence 58 from patent US 5538525.
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E34290 Phage and plasmid constructed by ligaring antibacterial protein gene DNA with vector DNA, transformant microorganism and transformant plant containing the same and antibacterial protein. E34290. I GI:18624295
DP 2000116379-A/1.
Unidentified unidentified unidentified unidentified unidentified unidentified unidentified unidentified.
                                                                                                                                                                                                                                                                                                Shoji,K.
Phage and plasmid constructed by ligating antibacterial protein gene DNA with vector DNA, transformant microorganism and transformant blant containing the same and antibacterial protein Patent: JP 2000116379-A 1 25-APR-2000;
TOTAMA PREF
OS Raphanus sativus L.
PN JP 2000116379-A/1
PD 25-APR-2000
PP 09-OCT-1998 JP 1998288472
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C12N15/09,A01H5/00,A01N65/00,C07K14/415,C12N1/21,C12N5/10//
(C12N15/09,C12R1:91),(C12N1/21,C12R1:19),(C12N5/10,C12R1:91), F
   SM Unknown.
Unclassified.

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La (bases 1 to 308)

RS lidang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.

Antifungal polypeptide AlvAPP from Alyssum and methods for controlling plant pathogenic fungi

NAL Patent: US 6653280-A 5 25-NOV-2003;

LCacation/Qualifiers

1.308

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C12N15/00,
PC C12N5/00, (C12N15/00, C12R1:91), (C12N5/00, C12R1:91)
FH Key
Location/Qualifiers
Locations
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Location/Qualifiers
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Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
Antifungal polypeptide and methods for controlling plant pathogenic
                                                                                                                                                                                                                                                                                                            linear PAT 05-DEC-1998
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Patent: US 5773696-A 5 30-JUN-1998;
Location/Qualifiers
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Squence 5 from patent US 5773696.
AR014682. GI:3972136
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Sequence 5 from patent US 6653280.
AR432382 AR432382.1 GI:40194659
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Terras, F.R.G., Eggermont, K., Kovaleva, V., Raikhel, N.V., Osborn, R.W., Keeler, A., Rees, S.B., Torrekens, S., Van Leuven, F., Vanderleyden, J., Cammue, B.P.A. and Brockaert, W.F. Small cysteine-rich antifungal proteins from radish: their role in host defense

Plant Cell 7, 568-573 (1995)
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Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
of Genetics, Applied Biological Sciences, W. De Croylaan 42,
Heverlee, Belgium, B-3001
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 191 AAGAATCAGTGCATTCGACTTGAGAAAGCACGACATGGGTCTTGCAACTATGTCTTCCCA 250
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Raphanus sativus
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129. .281
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sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
Chem. 267, 15301-15309"
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Cloned 3'
                                                                        Wasabia j
Brassica
                                                                                               Wasabia j
                                                                                                                                                                                                                                                                                                                                                         Truncated
                                                                                                                                        Arabidops
                     3rassica
                                                   Raphanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                                                                                                                Aav10632
Abz124 4
Abz124 4
Abz125 4
Abz42136 Aav10633
Aav10633 Aav29337 1
Aac94534
Aac94534
Aac99332 Aac99332 Aac99332 Aac99332 Aac99333
                                                                                                                                                                                                                                                         Aaz99329
Aaz99333
Aaz99335
Aaz99338
Aaz99336
Aaz99339
Aaz99334
                                                                                                                                                                                                                                                                                                                                                                   Aaq70129
Aat94580
                                                                                                                                                                                                                                                                                                                                                        Aaq38651
                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
AAZ99326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ICIL ) IMPERIAL CHEM IND PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92GB-00003038.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92GB-00013526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ38652 standard; DNA; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16. .256
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raphanus sativus.
Rs-AFP2 CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9305153-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ38652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ38652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aaq38652 Rs-AFP2 c
Aaq70130 Antimicro
Aat48577 Cloned 5 '
Aaa53190 Raphanus
Aaz53324 DNA encod
Aaz51396 Portion o
Aaz99325 DNA encod
Aaz99325 DNA encod
                                                                      May 13, 2004, 09:41:12; Search time 349 Seconds (without alignments) 608.624 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                       1 KLCERSSGTWSGVCGNNNAC.....QHGSCNYVFPAHKCICYFPC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                    OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                           3373863 seqs, 2124099041 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ51396
AAZ99327
AAZ99325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT94577
AAA53190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ38652
                                                                                                                                                                    Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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genesequ2000s: *
genesequ2001as: *
genesequ2001bs: *
genesequ2003s: *
genesequ2003as: *
genesequ2003as: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    geneseqn2004s:*
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                                                                                                                  US-10-006-252A-10
                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                               Perfect score:
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                                                                                                                                         Sequence:
                                                                          Run on:
                                                                                                                   Title:
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Cammue BPA, Osborn RW, Rees SB, Terras FRG; Broekaert WF, ( Vanderleyden J;

WPI; 1993-100978/12.

Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial diseases.

Example 21; Fig 35; 110pp; English.

This cDNA represents the sequence of Rs-AFP2 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 123bp product, which was further reamplified with the same primers and closxigenin-11-dUTP instead of further reamplified with the same primers and product. This was used to screen a lambda ZAPII cDNA library by in situ plaque hybridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage R408.Inserts from 2 positive clones were excised by Bcorl digstion and insert sizes of approx. 400bp the others between 250-300bp. The inserts of the 4 largest clones were then sequenced and found to differ only in the length of their s' and 3' UTR's. The longest sequence was identified as Rs-AFPI so their S' and 3' UTR's. The longest sequence was identified as Rs-AFPI so the Rs-AFPI cDNA was transformed to the Rs-AFPI concepting sequence by PCR assisted site directed mutagenesis. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;

Conservative: Mismatches: Indels: Length: Matches: 3.516-26 281.00 96.00% 92.00% 93.36% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match:

## 106 AAGTIGTGCCAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGGAAACAATAACGCATGC 165 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys US-10-006-252A-10 (1-50) x AAQ38652 (1-261) 8

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166 AAGAATCAGTGCATTAGACTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 225

RESULT 2

AAQ70130 standard; cDNA; 288 BP

(first entry) (revised) 25-MAR-2003 14-FEB-1995 AA070130:

Antimicrobial Rs-AFP2.

SX XX XX XX BX XI DX X Y

Antifungal polypeptide, AlyAFP, inhibition, transgenic plants, phytopathogenic fungus, resistance, ss.

WO9737024-A2 09-0CT-1997

Alyssum sp.

Antimicrobial; Rs-AFP2; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; PCR; polymerase chain reaction; mutagenesis; ss.

Raphanus sativus.

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Plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA sequence of PCR assisted site-directed mutagenesis of Rs-AFP2 is given in AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 AAGTIGIGCCAAAGGCCAÁGIGGGACAIGGICAGGAGTCIGIGGAAACAAAAA 6GCAIGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LysleuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloned 5' region of antifungal polypeptide cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 GCTCACAAGTGTATCTGCTACTTTCCTTGT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 AlaHisLysCysIleCysTyrPheProCys 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-006-252A-10 (1-50) x AAQ70130 (1-288)
                                                                                                                                                                                                                                                                                           Disclosure; Page 33; 39pp; English.
                                                                                                                                                          Dubock AC, Powell KA, Rees SB;
                                                                                                                                                                                                                                                                                                                                                                                                               MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT94577 standard; DNA; 308 BP.
                                                                     94WO-GB000012.
                                                                                                  93GB-00000281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281.00
96.00%
92.00%
93.36%
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                                                                                                                                                                                      WPI; 1994-249223/30.
                                                                                                                               (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity:
                                                                                                                                                                                                      P-PSDB; AAR57327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                    05-JAN-1994;
                                                                                                  08-JAN-1993;
            WO9416076-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                         21-JUL-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT94577;
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DB:
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#X#X#X#X#X###X#X#X

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Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
protein expression; plant defensin; RSAFP2; antifungal protein; AFP2; ss
                  Isolated DNA from Raphanus sativus used to transform a microbe and a plant to produce an antibacterial protein used to increase resistance of rice paddy against pathogenic microbes.
                                                                                                       The present sequence encodes an antibacterial protein, designated radishin, isolated from Raphanus sativus (radish). A phage or plasmid comprising radishin can be used for increasing resistance of paddy and rice blast disease against pathogenic microbes
                                                                                                                                                                                                                                                                                                                                                        21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding a fusion protein of DmAMP1 and RSAFP2.
                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 GCTCACAAGTGTATCTGTTATTTCCCTTGT 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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/*tag= a
/note="encodes DmaMP1"
358. 510
/*tag= b
/note= "encodes RsAFP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 AlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                US-10-006-252A-10 (1-50) x AAA53190 (1-449)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
                                                                                 Claim 1; Page 4; 7pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-GB002716.
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281.00
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Best Local Similarity:
P-PSDB; AAY91117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dahlia merckii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-AUG-1998;
04-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc feature
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                                                                                                                                                                                                                 Alignment Scores:
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DB:
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No
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RXFFFXXXXCCCXX
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                                                                                                                                                                                                                 This sequence is the product of the amplification of the 5' region of the antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum, by a 5' RACE (Rapid Amplification of cDNA Ends) using primers AAT94575-T94576). The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;
pathogenic microbe; radish; rice blast disease; ds.
                                                                                                                                             Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                      G; 79 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                             308
1146
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                      Rosenberger CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-006-252A-10 (1-50) x AAT94577 (1-308)
                                                                                                                                                                                          Example 4; Page 65; 92pp; English
                                                                                                                                                                                                                                                                                                                                      78 A; 71 C; 78
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    97WO-US005709
                               96US-00627706
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                                                                                        Shah D, Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-389821/34.
                                                                                                                 WPI; 1997-503109/46.
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                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                      BP;
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                                                            (MONS ) MONSANTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP2000116379-A.
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                                                                                                                                                                                                                                                                                                                                       Sequence 308
    27-MAR-1997;
                               29-MAR-1996;
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Query Match:
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us-10-006-252a-10.rng

Ray JA;

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The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMPP) I and the antifungal protein (AMPP). Inked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is postranslationally processed into the component protein molecules. The propeptide sequence is rich in anaho acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one codic and one basic residue as a cleavable linker sequence
                                                                                                                        Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.
  Evans 1J,
  De Bolle MFC,
                                                                                                                                                                                                      Example 2; Fig 8; 151pp; English
Broekaert WF, Francois IEJA,
                                             WPI; 2000-246564/21.
P-PSDB; AAY84057.
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## Sequence 522 BP; 147 A; 119 C; 127 G; 129 T; 0 U; 0 Other;

AAZ51396 standard; DNA; 534 BP. 06-JUN-2000 AAZ51396; 

(first entry)

Portion of pFAJ3106 encoding Dahlia merckii antimicrobial protein.

Antimicrobial protein, DmAMP, transgenic plant; microbial infection; bacteria; fungi, field crop; fruit; vegetable; canola; banana; sunflower; apple; plant transformation vector; ds.

Dahlia merckii. Synthetic.

Location/Qualifiers 76. .525 /\*tag= a /product= "Antimicrobial protein"

WO200011196-A1

```
The present sequence corresponds to the region between XhoI and SacI sites of plant transformation vector pFAJ3106, which encompass the coding region for Dahlia merckii antimicrobial protein, Dm-AMPI. The vector is useful in the production of transgenic plants which show improved resistance to infections by microorganisms such as bacteria and fundi. Transgenic plants include e.g. field crops, fruits and vegetables, such as canola, sunflower, tomato, apple, banana, pear and mango
                                                                                                                                                                                                                       Polynucleotide sequences and expression products useful for producing transgenic plants that are resistant to microbial infections.
                                                                                                                                                                                                                                                                      Example 3; Fig 7; 77pp; English.
                                99WO-GB002720
                                                                                                                                                                  WPI; 2000-237658/20.
P-PSDB; AAY70323.
                                                                                                 (ZENE ) ZENECA LTD.
                                                                                                                                  Evans IJ, Ray JA;
                              17-AUG-1999;
02-MAR-2000
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53 4 6 4 6 0 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: US-10-006-252A-10 (1-50) x AAZ51396 (1-534) 8.76e-26 281.00 96.00% 92.00% Percent Similarity: Best Local Similarity: Query Match: DB: ò

Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;

Alignment Scores:

433 AAGAATCAGTGCATTAGACTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 492 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40 à

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AAZ99327 standard; DNA; 534 BP AAZ99327; RESULT 7 THE HAND WAR AND THE HAND TO A WAR AND THE HAND THE HAND

(first entry) 03-JUL-2000

DNA encoding a fusion protein of DmAMP1 and RsAFP2.

Antimicrobial protein; AMP1; transgenic plant; linker propeptide; protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.

Synthetic. Dahlia merckii. Unidentified.

Location/Qualifiers

misc\_feature

/\*tag= a 162. 309 /\*tag= b /mote= "encodes DmAMP1"

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The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) I and the antifungal protein 2 (APP2), linked by a linker propertied of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                   Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.
                                                                                                                                                                                                                                Ray JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 534 BP; 154 A; 120 C; 125 G; 135 T; 0 U; 0 Other;
                                                                                                                                                                                                                                Evans IJ,
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Matches:
Conservative:
Mismatches:
Indels:
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372. .519
/*tag= c
/note= "encodes RSAFP2"
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                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 12; 151pp; English.
                                                                                                                                                                                                                                 Francois IEJA,
                                                                                                                         99WO-GB002716.
                                                                                                                                                      98GB-00018001
98GB-00026753
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281.00
96.00%
92.00%
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                                                                                                                                                                                                 (ZENE ) ZENECA LTD.
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                                                                                                                                                                                                                                                                             P-PSDB; AAY84060.
                                                            WO200011175-A1
                                                                                                                                                                                                                                Broekaert WF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                         17-AUG-1999;
                                                                                                                                                      18-AUG-1998;
04-DEC-1998;
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Pred. No.:
    misc_feature
                                                                                           02-MAR-2000
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DB:
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The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) 1 and the antifungal protein 2 (AFP), linked by a linker propertide of the invention. The specification describes methods for the invention. The specification describes methods for expense the reading operably linked to two or more proteins in a transgenic plant. The method comprises inscrting a DNA sequence having a promoter egglon operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is posttranslationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dispeptide; sequences consisting of either two addict, two basic or one
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protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ray JA;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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160. .399
/*tag= b
/note= "encodes DmAMP1"
370. .538
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Francois IEJA,
                                                                                                                                                                                                                                                                                                                                                                              98GB-00018001.
98GB-00026753.
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96.00%
92.00%
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Best Local Similarity:
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                                                          Synthetic.
Dahlia merckii.
Unidentified.
                                                                                                                                                                                                                                                                                   WO200011175-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Broekaert WF,
                                                                                                                                                                                                                                                                                                                                                  17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                18-AUG-1998;
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                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                       misc feature
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Query Match:
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AAZ99326 standard; DNA; 606 AAZ99326

(first entry) 03-JUL-2000

DNA encoding a fusion protein of DmAMP1 and RSAFP2.

Antimicrobial protein; AMP1; transgenic plant; linker propeptide; protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.

Synthetic. Dahlia merckii. Unidentified.

Location/Qualifiers 76. .597 Key

/\*tag= a | /\*tag= b | /\*tag= b | /\*tag= b | /\*tag= codes DmAMP1" | /\*tag= c | misc\_feature

misc\_feature

WO200011175-A1

02-MAR-2000

99WO-GB002716 17-AUG-1999;

98GB-00018001 98GB-00026753 18-AUG-1998; 04-DEC-1998;

(ZENE ) ZENECA LTD.

Ray JA; Evans IJ, De Bolle MFC, Sroekaert WF, Francois IEJA,

WPI; 2000-246564/21 P-PSDB; AAY84059.

Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.

Example 2; Fig 11; 151pp; English

The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker properied of the invention. The specification describes methods for improperied of the invention. The specification describes methods for plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is posttranslationally processed into the component protein molecules. The propeptide sequence is rich in amino acide A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence 

Sequence 606 BP; 189 A; 136 C; 137 G; 144 T; 0 U; 0 Other;

	909	46	
	Length:	Matches:	
	1.03e-25	281.00	
Alignment Scores:	Pred. No.:	Score:	

Conservative: 2 Mismatches: 2 Indels: 0 Gaps: 0	-606)	1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys 20	445 AAGTTGTGCCAAAGGCCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 504	21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40	505 AAGAATCAGTGCATTAGACTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 564	2roCys 50	CTTGT 594
Percent Similarity: 96.00% Best Local Similarity: 92.00% Query Match: 93.36% DB: 3	US-10-006-252A-10 (1-50) x AAZ99326 (1-606)	Qy 1 LysLeuCysGluArgSerSerGly'	DD 445 AAGTTGTGCCAAAGGCCAAGTGGG	Oy 21 LysAsnGlnCysIleArgLeuGlu	Db 505 AAGAATCAGTGCATTAGACTTGAGA	Oy 41 AlaHisLysCysIleCysTyrPheProCys 50	Db 565 GCTCACAAGTGTATCTGCTACTTTCCTTGT 594

ABQ82690 standard; cDNA; 243 AB082690;

RESULT 10

(first entry) 02-JAN-2003 Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:1.

Wasabia japonica, gamma-thionin, plant, disease-resistant plant, gene,

wasabi Eutrema Location/Qualifiers
1. .243
/\*tag= a
/product= "gamma-thionin"

JP2002272292-A

24-SEP-2002

22-MAR-2001; 2001JP-00083526

22-MAR-2001; 2001JP-00083526.

(IWAT-) IWATE KEN

WPI; 2002-718704/78. P-PSDB; ABP53725.

A disease-resistant plant in which wasabi gamma-thionin gene is introduced, creation of the disease-resistant plant.

Claim 3; Page 8; 11pp; Japanese.

The present invention describes a disease-resistant plant in which a wasabi gamma-thionin gene is introduced. Also described is a method for the creation of the above disease-resistant plant by introducing a wasabi gamma-thionin gene to a plant. The present sequence encodes a Butrema wasabi (Wasabia japonica) gamma-thionin protein from the present invention 

BP; 60 A; 54 C; 55 G; 74 T; 0 U; 0 Other; Sequence 243

Alignment Scores:			
Pred. No.:	5.69e-26	Length:	243
Score:	279.00	Matches:	44
Percent Similarity:	\$00.96	Conservative:	4
Best Local Similarity:	88.00%	Mismatches:	7
Query Match:	92.69%	Indels:	0
DB:	9	Gaps:	0

m 0 0

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This cDNA represents the sequence of Rs-AFP1 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for. screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 123bp product, which was further reamplified with the same primers and digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII cDNA library by in situ plaque hybridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage
                                                                                                                                    91 AAGTTGTGCAAGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 150
                                                                                                                                                                                                                     of plants - e.g. brassica or resistance to fungal and bacterial
                                                                                                                   1 LysleuCysCluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                                                             21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rees SB,
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                        211 GCTCACAAGTGTATTTGCTACTTCCCTTGT 240
                                                                                                                                                                                                                                                                                  41 AlaHisLysCysIleCysTyrPheProCys 50
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                                        Gaps:
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                                                                            US-10-006-252A-10 (1-50) x ADC51221 (1-394)
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                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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92.00%
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    Similarity:
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Vanderleyden J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
07-JUL-1993
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  Best Local Si
Query Match:
DB:
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                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
                                                                                     91 AAGTTGTGCGAGAAACTCAAGTGGACATGGTCAGAGTCTGTGGAAACAACAATGCGTGC
                                                                                                                                            21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
                                                               1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Brassica oleracea defensin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antimicrobial protein; defensin; transgenic plant; composite disease resistance; pathogenic bacteria; rice white leaf blight, brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;
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46
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica oleracea defensin protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                     211 TATCACAGATGTATCTGTTACTTCCCATGT 240
                                                                                                                                                                                                                           41 AlaHisLysCysIleCysTyrPheProCys 50
                         US-10-006-252A-10 (1-50) x ABQ82690 (1-243)
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                                                                                                                                                                                                                                                                                                                                                       ADC51221 standard; DNA; 394 BP
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279.00
94.00%
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P-PSDB; ADC51222.
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Brassica oleracea.

18-DEC-2003

ADC51221;

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셤 à g 8 JP2003088379-A.

25-MAR-2003

Terras FRG;

Conservative:

Percent Similarity:

Alignment Scores:

R408.Inserts from 22 positive clones were excised by EcoRI digestion and their size compared by agarose gel electrophoresis. Four clones had insert sizes of approx. 400bp the others between 250-300bp. The inserts of the 4 largest clones were hen sequenced and found to differ only in the length of their 5' and 3' UTR's. The longest sequence is given here. (Updated on 25-MAR-2003 to correct PN field.) 8888888888

Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

414 146 00 00 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.12e-25 279.00 94.00% 92.00% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB:

US-10-006-252A-10 (1-50) x AAQ38650 (1-414)

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106 AAGITGTGGGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGC 165 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys н

20 41 AlaHisLysCysIleCysTyrPheProCys

AAQ70128 standard; cDNA; 414 (revised)
(first entry) 25-MAR-2003 14-FFB-1995 AAQ70128;

Antimicrobial Rs-AFP1

Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.

Raphanus sativus.

WO9416076-A1

21-JUL-1994

94WO-GB000012. 05-JAN-1994;

93GB-00000281 08-JAN-1993;

(ZENE ) ZENECA LTD

Powell KA, Dubock AC,

WPI; 1994-249223/30. P-PSDB; AAR57325 Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.

Disclosure; Page 31; 39pp; English.

Plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodoniis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFPI from R. sativus. The full-length cDNA sequence of Rs-AFPI is given in AAQ70128. (Updated on 25-MAR-2003 to 

414 46 1 3 3 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: 20 226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 41 AlaHisLysCysIleCysTyrPheProCys US-10-006-252A-10 (1-50) x AAQ70128 (1-414) 1.12e-25 279.00 94.00% 92.00% Similarity: Percent Similarity: Best Local Similari Alignment Scores Query Match: DB: 9 ò ò 8

Other;

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Sequence 414 BP; 128 A; 74

correct PN field.)

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ВР AAT72333 standard; cDNA; 414

AAT72333;

(first entry) (revised) 25-MAR-2003 19-JAN-1998

Antifungal protein; candida; fungal resistance; food additive; radish; crop protection; plant defensin; bacterial protection; preservative; ss.

Raphanus sativus antifungal protein I (Rs-AFP1) cDNA.

16. .256 /\*tag= a /transl\_except= (pos:85, .87, aa:Glu) 16. .102 /\*tag= b 103. .255 /product= "antifungal\_protein\_1" Location/Qualifiers sig\_peptide mat\_peptide 

WO9721815-A2

19-JUN-1997,

95GB-00025455. 96GB-00006552. 96WO-GB003068 12-DEC-1996; 13-DEC-1995; 28-MAR-1996;

(ZENE ) ZENECA LID.

Ä Meloen RH, Puijk WC, Schaaper WAM, Sijtsma L, Van Amerongen Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB; Van Gelder WMJ;

WPI; 1997-332786/30. P-PSDB; AAW19280 Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.

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This cDNA sequence encodes an Rhapanus sativus (radish) antifungal protein (Re-AFPZ). Analogues of the homologous protein. Rs-AFPZ AAM19281), have also been produced (see AAM19282-92, AAM19394-98, AAM19301-04, AAM19330-34 and AAM31765-834). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease tolerance of crops, either pre or post harvest. When applied to plants they may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorganism capable of expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct plied).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 AAGTIGIGGAAAAGGCCAAGIGGGACAIGGICAGGAGICIGIGGAAACAAIAACGCAIGC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rs-AFP1; radish antifungal protein 1; fungicide; salt tolerance; preservative; transgenic plant; crop protection.
                                                                                                                                                                                                                                                                        Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rtag= a
/transl_except= (pos:85. .87, aa:Glu)
16. .102
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Radish antifungal protein 1 (Rs-AFP1) cDNA.
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              Claim 8; Fig 2; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                                         New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
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Matches:
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Indels:
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                                                                                                                                                                                              Disclosure; Fig 2; 39pp; English
                                                  Broekaert WF, De Samblanx GW,
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                                                                                     1997-332785/30.
               (ZENE ) ZENECA LTD.
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Job time : 350 secs
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APPLICANT: Liang, Jihong
APPLICANT: Stah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Clindy A.
APPLICANT: Rosenberger, Clindy A.
APPLICANT: Rosenberger, Clindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STRAEE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
             US-08-777-1924-48
US-08-777-1924-48
US-08-971-982-48
US-09-107-9488-45
US-09-107-9488-45
US-09-103-489-14
US-09-103-489-12
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NAME: Cohen, Charles B.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10700) A
TELECOMMUNICATION INFORMATION:
TELEPAX: (314)537-624
TELEPAX: (314)537-621
INFORMATION FOR SEQ ID NO: 17:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5773696
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CLASSIFICATION: 436
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RESULT 1
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58, Appl
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-103-489-17
US-09-2829-381D-17
US-08-377-687-58
US-08-777-192-58
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US-09-627-706-5
US-09-103-489-5
US-09-829-381D-5
US-09-103-489-16
US-09-103-489-16
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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/desc = "synthetic DNA'

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: ROSENDETGET, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 20
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PRECENTED RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UN-1998
CLASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 38-21 (10700)A
TELECOMMUNICATION INUMBER: 38-21
TELECOMMUNICATION INUMBER: 38-21
                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 AlaHisLysCysIleCysTyrPheProCys 50
                     LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (314) 537-6647
INPORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
                                                                                                                                                                            3.12e-28
281.00
96.00%
92.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                Alignment Scores:
                                                                                                                             US-08-627-706-17
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DB:
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Sequence 17, Application US/09829381D

Patent No. 6653280

GENERAL INFORMATION:
Patent No. 6653280

GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Rescherger, Cindy A.
APPLICANT: Rescherger, Cindy A.
TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE OF INVENTION: Plant Pathogenic Fungi
CURRENT FILING DATE: 2001-04-09

FRIOR APPLICATION NUMBER: 09/103,489

FRIOR APPLICATION NUMBER: 09/103,489

FRIOR APPLICATION NUMBER: 09/103,489

FRIOR PILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 20
SOFTWARE PatentIn Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                       1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
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Matches:
Conservative:
Mismatches:
Indels:
           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                          US-10-006-252A-10 (1-50) x US-09-103-489-17 (1-285)
                                                                                                                                                                                                                                                                                     241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 AlaHisLysCysIleCysTyrPheProCys 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.12e-28
281.00
96.00%
92.00%
           3.12e-28
281.00
96.00%
92.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Synthetic US-09-829-381D-17
                                        Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-09-829-381D-17
Alignment Scores:
Pred. No.:
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Pred. No.:
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LENGTH: 285
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DB:
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133 AAGTTGTGCCAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 192
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILLING DATE: 04-0AN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEBHOME: 202-861-300
TELEBHOME: 202-861-300
TELEBHOME: 202-822-0944
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC compactible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                             APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: UNDERLEYDEN, JOZEF
APPLICANT: LOSEPHMAN BARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                  SEE: CUSHMAN DARBY & CUSHMAN: 1100 NEW YORK AVENUE, N.W. WASHINGTON
                   Sequence 58, Application US/08777192; Patent No. 5824869; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.17e-28
281.00
96.00%
92.00%
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TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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Query Match:
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; LOCATION: 43.
US-08-777-192-58
                                                                                                                                                                                                                                                                                                                                                                                      CITY: WASHI)
STATE: D.C.
COUNTRY: US.
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US-08-777-192-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZINE: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MM-DOS
SOFTWARE: PETENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/377,687
FILING DATE: US/08/33
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 18,773
REFERENCE/DOCKET NUMBER: 1900
TELEFAX: 202-861-300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
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     Sequence 58, Application US/08377687
Patent No. 553825
GENERAL INFORMATION:
APPLICANT: BROEKABRT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: REES, SARAH B.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, SARAH B.
APPLICANT: TERRAS, SARAH B.
APPLICANT: TERRAS, SARAH B.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BICCIDAL PROTEINS
TITLE OF INVENTION: BICCIDAL PROTEINS
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN DARBY & CUSHWAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUTTRY: USA
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Query Match:
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LOCATION: 43.
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CARPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34.565
REFERENCE/DOCKET NUMBER: 38-21(10700) A
TELEPHONE: (314)537-624
TELEPHONE: (314)537-624
TELEPAX: (314)537-624
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8 4 4 6 0 0
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Matches:
Conservative:
Mismatches:
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94.00%
92.00%
93.36%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971.982
FILING DATE: 17-NO. 618/904-1997
CLASSIFICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELERAK: 202-861-3000
INFORMATION: COR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENTH: 28B base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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               Sequence 58, Application US/08971982
Patent No. 6187904
GENERAL INFORMATION:
CAMMUE, BRUNO P.A.
OSBONI, RUPERT W.
REES, SARAH B.
TERRAS, FRANKY R.G.
VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BLOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CUSHWAN DARBY & CUSHWAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 GCTCACAAGTGTATCTGCTACTTTCCTTGT 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 43..282
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.17e-28
281.00
96.00%
92.00%
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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Best Local Similarity:
Query Match:
DB:
US-08-971-982-58
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1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
                                                                         21 LysAsnGlnCysIleArgleuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                          RESULT 8
US-09-103-489-5
Sequence 5, Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
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219 AAGAATCAGTGCATTAACCTTGAAGGAGCNCGACATGGATCTTGCAACTATGTCTTCCCA 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Nonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STRATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308
46
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                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic PCR reaction product FEATURE:
NAME/KEY:
LOCATION: (22)...(248)
OTHER INFORMATION: N = any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-006-252A-10 (1-50) x US-09-829-381D-5 (1-308)
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Gaps:
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REFERENCE/DOCKET NUMBER: 38-21(10700)A
TELECOMOUNICATION:
TELEPHONE: (314)537-6224
PRIOR APPLICATION NUMBER: 09/103,489
FRICR PILING DATE: 1908-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LINGHH: 308
TUDNGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08627706
Patent No. 5773696
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.46e-28
281.00
94.00%
92.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-829-381D-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-627-706-16
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                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NS-00-829-381D-5
Sequence 5, Application US/09829381D
Sequence 5, Applicant Interpretation US/09829381D
Sequence 6, Applicant Interpretation US/09/829, 381D
Sequence 6, Application US/09/829, 381D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 AAGTIGIGGAGAGTCCAAGIGGAACAIGGICAGGCGIGIGIGGAAACAACAAGAIGCIIGC 218
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                         APPLICANT: Wu. Yonnie S.

PEPLICANT: Wu. Yonnie S.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF EXCURNICAS: 20 CORRESPONDENCE ADDRESS:

ADDRESSEB: Charles E. Cohen, Monsanto Company, BB4F STREET: 700 Chesterfield Village Parkway No. 6215048th
                                                                                                                                                                                                                                     AUDKESSEE: Charles E. Cohen, Monsanto Company, BB4
STREET: 700 Chesterfield Village Parkway No. 62150
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 4-JUN 1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: COHEN, Charles E.
REGISTRATION NUMBER: 34.565
REFERENCE/DOCKET NUMBER: 34.565
REPRENCE/DOCKET NUMBER: 34.565
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Matches:
Conservative:
Mismatches:
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TYPE: nucleic acid
STRANDEDNESS: single
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94.00%
92.00%
93.36%
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US-09-103-489-5
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
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TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic DNA"

US-09-103-489-16

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1 LysleuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Rw, Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F STREET: 700 Chesterfield Village Parkway No. 6215048th CITY: St. Louis STATE: Missouri
                                                                                                                                                                                                                   285
1 4 6
0 0
0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
COMPUTER: IBM PC Compartible
COMPATATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UUN-1998
CLASSIFCATION: 800
                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                   US-10-006-252A-10 (1-50) x US-08-627-706-16 (1-285)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION UNDERS: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEPHONE: (314) 537-6224
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: CASS base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                          MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic DNA"

US-08-627-706-16
TELEFAX: (314)53-6047
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 285 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                 5.69e-28
279.00
94.00%
92.00%
                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-103-489-16
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121 AAGTTGTGCGAGAGGCCATCAGGGACTTGGTCAGGAGTCTGCGGAAACAACAACGATGC 180
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                                                                                              1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-006-252A-10 (1-50) x US-09-829-381D-16 (1-285)
                                                                            US-10-006-252A-10 (1-50) x US-09-103-489-16 (1-285)
                                                                                                                                                                          41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic US-09-829-381D-16
                 279.00
94.00%
92.00%
92.69%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279.00
94.00%
92.00%
92.69%
                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                             US-09-829-381D-16
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                           Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 AAGTIGIGGAAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC
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9 4 6 0 0
0 0 0 0
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CLASSIFICATION:
PLICASTIFICATION
PLOST APPLICATION
PROBLICATION DATA:
APPLICATION NUMBER: US 08/002,480
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/ADCKET NUMBER: 16,773
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPL/CATION DATA:
APPL/CATION NUMBER: US/08/777,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-006-252A-10 (1-50) x US-08-777-192-48 (1-414)
226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                        APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAWNUE, BRUNO P.A.
APPLICANT: CABORN, RUPERT W.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                       STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: US' ZION
                                                                                    Sequence 48, Application US/08777192
Patent No. 5824869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.24e-28
279.00
94.00%
92.00%
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16..255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . LOCATION:
US-08-777-192-48
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 LysaksnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAM-1993
ATTONNEY AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMNUNICATION INFORMATION:
TELECOMNUNICATION INFORMATION:
TELEFAX: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-006-252A-10 (1-50) x US-08-377-687-48 (1-414)
241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 AlaHisLysCysIleCysTyrPheProCys 50
                                                      US-08-377-687-48

Sequence 48, Application US/08377687

Parent No. 5284525

GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CANVUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: CUSHWAN DARBY & CUSHWAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.24e-28
279.00
94.00%
92.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16..255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
US-08-377-687-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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165

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Search completed: May 13, 2004, 12:19:39 Job time: 88 secs

g GENERAL INFORMATION:

APPLICANT: BROCEAGERT, WILLEM F.

CAMMUD. BRUND P.A.

CAMMUD. BRUND P.A.

SEES, SARAH B.

TERRAS, FRANKY R.G.

VANDERLEYDEN, JOZEF

TITLE OF INVENTION: BIOCIDAL PROTEINS

NUMBER OF SEQUENCES: 59

CORRESSED CUSHWAN DARRY & CUSHWAN

STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON

STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON

STREET: 100 NEW YORK AVENUE, N.W.

COUNTRY: USA

ILE OF SEQUENCES: 59

COMPUTER: EDG.

CONFUTER: EDG.

CONFUTER: EDG.

CONFUTER: EDG.

CONFUTER: EDG.

CONFUTER: EDG.

SOFTWARE: PRECIDENCE

CONFUTER: DATE: 0.005

SOFTWARE: PRECIDENCE

CONFUTER: DATE: 0.005

SOFTWARE: PRECIDENCE

CONFUTER: DATE: 0.005

SOFTWARE: DATE: 0.005

SOFTWARE: DATE: 0.005

SOFTWARE: DATE: 0.005

FILING DATE: 0.007

PRIOR APPLICATION NUMBER: 0.004

APPLICATION NUMBER: 0.007

PRIOR APPLICATION NUMBER: 0.007

APPLICATION NUMBER: 0.007

REGISTRATION NUMBER: 0.007

TELEPRONE YAGEN INFORMATION:

NAME: XOKULIS, PAUL N.

REGISTRATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 414 base pairs

TONOLGOTICST: Hinear

MOLECULG TYPE: CDNA

MOLECULE TYPE: CDNA

PETATURE: PETATURE:

PEATURE:

PEATURE:

PEATURE:

PEATURE:

PEATURE:

PEATURE:

PEATURE:

PEATURE:

PEATURE:

NAME: CDNA

MANE: CDNA

MOLECULG TYPE: CDNA

PETATURE:

PEATURE:

PEATURE 226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255 ), NAME/KEY: CDS ; LOCATION: 16.255 ; SEQUENCE DESCRIPTION: SEQ ID NO: 48: US-08-971-982-48 RESULT 15
US-06-971-982-48
Sequence 48, Application US/08971982
Patent No. 6187904
CENERAL INCRNATION:

US-10-006-252A-10 (1-50) x US-08-971-982-48 (1-414)

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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

9.24e-28 279.00 94.00\$ 92.00\$

Score:
Percent Similarity:
9
Best Local Similarity:
9
Query Match:
3

Alignment Scores: Pred. No.:

41 AlaHisLysCysIleCysTyrPheProCys 50

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Sequence 17, Appl Sequence 5, Appl Sequence 5, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 13, Appl Sequence 2046, Appl Sequence 21, Appl Sequence 21, Appl Sequence 11, Appl Sequence 12, Appl Sequence 3, Appl Sequence 33, Appl Sequence 34, Appl Sequence 36, Appl Sequence 37, Appl Sequence 37, Appl Sequence 15, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Appl
Sequence 33, Appl
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Appl:
Sequence 19, Appl
Sequence 23, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17,
Sequence 46,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
                                                       9 US-09-759-584-58

13 US-10-681-972-5

9 US-09-829-381A-16

9 US-09-829-381A-16

9 US-09-829-584-48

13 US-10-681-972-6

9 US-09-938-847A-2046

9 US-09-732-561-12

9 US-09-732-561-12

9 US-09-732-561-12

9 US-09-732-561-12

9 US-09-938-847A-2046

9 US-09-938-847A-2046

9 US-09-938-847A-2046

9 US-09-938-847A-2046

9 US-09-938-847A-14

13 US-10-181-12

14 US-10-181-12

15 US-09-829-381A-9

16 US-09-829-381A-9

17 US-09-829-381A-9

18 US-10-681-972-12

19 US-09-829-381A-9

10 US-09-829-381A-9

10 US-09-829-381A-9

11 US-10-178-449A-31

12 US-10-178-449A-15

15 US-10-178-449A-17

16 US-10-178-449A-17

17 US-10-178-449A-17

18 US-10-178-449A-17

19 US-09-759-584-34

10 US-09-759-584-34

11 US-10-178-449A-17

12 US-10-178-449A-17

13 US-10-178-449A-17

14 US-10-178-449A-17

15 US-10-178-449A-17

16 US-09-759-584-34

17 US-09-759-584-34

18 US-09-759-584-34

19 US-09-759-584-34
     US-09-829-381A-17
US-10-681-972-17
US-09-759-584-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 63198
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                            US-09-829-381A-17
        Command line parameters:
-MODEL=frame+-p21.model -DEV=xlp
-MODEL=frame+-p21.model -DEV=xlp
-MODEL=frame+-p21.model -DEV=xlp
-DES-published Applications NA -QFNT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-DES-published Applications NA -QFNT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPELS -O. -LOOPEXT=0 -UNITE=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFNT=pcto -NORM=ext -HEARSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=USI0006252 @CGN i 1 333 @runat 11052004 141949 11000
-LONGLGG -DEV TINEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOF=10 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                  (without alignments)
68.324 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                301
1 KLCERSSGTWSGVCGNNNAC.....QHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12. (cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

12. (cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

13. (cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

14. (cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

15. (cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

16. (cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

17. (cgn2_6/ptodata/1/pubpna/DSO8_PUBCOMB.seq:*

18. (cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

19. (cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

10. (cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

11. (cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

12. (cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

13. (cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

14. (cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

15. (cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

16. (cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

17. (cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

18. (cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

19. (cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

10. (cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

11. (cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

12. (cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

13. (cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

14. (cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

15. (cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

16. (cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

17. (cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

18. (cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

18. (cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

19. (cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

10. (cgn2_6/ptodata/1/pubpna/USO0_PU
                                                                                                                                                                        ; Search time 3321 Seconds
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                      nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2947324 segs, 2269024515 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                   Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                     May 13, 2004, 11:00:48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                   US-10-006-252A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length
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Database

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Total number

Searched:

Scoring table:

Perfect score:

Title:

Sequence:

OM protein -

Run on:

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ОВ

Score

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Result

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21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                             1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                             242
86
85
85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUDNITKY: USA

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: THE PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                  US-10-006-252A-10 (1-50) x US-10-681-972-17 (1-285)
                                                                                                                                                                                                                                                                                                                     41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                             Sequence 58, Application US/09759584
; Sequence 58, Application US/09759584
; Patent No. US20010014732A1
; APPLICANT: BROEKABET, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: CAMMUE, RUEBET W.
APPLICANT: RES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN NATURE.
                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
      , OTHER INFORMATION: Synthetic US-10-681-972-17
                                                                           281.00
96.00%
92.00%
93.36%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                          Percent Similarity:
Best Local Similarity:
                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                        Query Match:
                                                                  Pred. No.:
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121 AAGTTGTGCCAAAGGCCATCAGGAACTTGGTCAGGAGTCTGCGGAAACAACAACGATGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-006-252A-10 (1-50) x US-09-829-381A-17 (1-285)
                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-09-829-381A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO. 17:
SEQUENCE CHARACTERISTICS:
LENGH: 285 Base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                              6.96e-31
                                                                                                                                                                                                                                                                                                                                                                                                                          281.00
96.00%
92.00%
93.36%
                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                   193 AAGAATCAGTGCATTAGACTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 252
                                                                                                                                                                                                                                                                                                                                            21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                               1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/829,381A

FILING DATE: 09-Apr-2001

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 09/103,489

FILING DATE: 1998-06-24

ATTORNEY/AGENT INPORMATION:

NAMM: COHON. Charles E.

NAMM: COHON. Charles E.

NAMM: COHON. Charles E.

REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700) A

TELLEFAX: (314) 537-6224
                                                                              04000
80
80
                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 GCTCACAAGTGTATCTGCTACTTTCCTTGT 282
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LENGTH: 308 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECTIE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-829-381A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS
                                                                    7.06e-31
281.00
96.00%
92.00%
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  43..282
                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                           Alignment Scores:
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US-09-829-381A-5
LOCATION:
    , LUCATION:
US-09-759-584-58
                                                                              Pred. No.:
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                                                                                                              1 iyşiçeüÇyşGlüArgSerŞerGlYThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
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          Length:
Matches:
Conservative:
Mismatches:
Indels:
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FEATURE:
NAME/KRY: misc feature
COCATION: (22)...(248)
COTHER INFORMATION: N = any nucleotide
US-10-681-972-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                              41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
          7.7e-31
281.00
94.00%
92.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7e-31
281.00
94.00%
92.00%
                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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Alignment Scores:
Pred. No.:
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41 AlaHisLysCysIleCysTyrPheProCys 50

Page

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ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LysleuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys 20
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                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                   APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

REDIUM TYPE: Floppy disk
COMPUTER: TYPE: Floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <u >CLASSIFICATION</u>
CLASSIFICATION: <u >cunknown></u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285
46
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APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:

NAME: Cohen, Charles E.

REGISTRATION NUMBER: 34,565
REFERAÇÃOCKET NUMBER: 38-21 (10700) A
TELECOMMUNICATION INFORMATION:

TELEFFAM: (314) 537-6224
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESCRIPTION: /desc = "synthetic DNA sequence DESCRIPTION: SEQ ID NO: 16:
241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthet
                                                                                            Sequence 16, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.34e-30
279.00
94.00%
92.00%
                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                    CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                US-09-829-381A-16
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DB:
                                                           RESULT 6
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Sequence 16, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE OF INVENTION: 10.000 C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR FILING DATE: 2003-10-09
PRIOR FILING DATE: 09/103,489
PRIOR FILING DATE: 1999-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AAGAACCAATGCATCAACCTCGAGAAGGCACGGCATGGATCTTGCAACTACGTCTTCCCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CASARN, RUESTY W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: VANDERLEYDEN, JOZEF
ANDERSESE: CUSHWAN DARBY & CUSHWAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 48, Application US/09759584 Patent No. US20010014732A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.34e-30
279.00
94.00$
92.00$
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic US-10-681-972-16
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 20
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Percent Similarity:
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Pred. No.:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
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COMPUTER: IBM PC compatible
SOSTAME: Patentin Release #1.0, Version #1.25
SOSTAMENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FILING DATE:
CLASSIFICATION NUMBER: US/09/759,584
FILING DATE:
APPLICATION NUMBER: 08/377,687
FILING DATE:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATCORNEY AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861.3000
TELEPHONE: 202-862.3004
TELEPHONE: 202-862.3004
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941
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Publication No. US20030226169A1
GRNERAL INFORMATION:
APPLICANT: Van Amerongen, Aart
APPLICANT: Fant, Franky
APPLICANT: Borremans, Frans
APPLICANT: Borremans, Frans
APPLICANT: Sifitsma, Lolke
APPLICANT: Sifitsma, Lolke
APPLICANT: Brokeart, Robbert
APPLICANT: Puilk, Wouter
APPLICANT: Brokeart, Wilhelmus
APPLICANT: Brokeart, Wilhelmus
APPLICANT: Brokeart, Wilhelmus
APPLICANT: Van Gelder, Wilhelmus
APPLICANT: Van Gelder, Wilhelmus
APPLICANT: Rees, Sarah
ITILE REFERRUCE: 50094PPDDIV
CURRENT FILING DATE: 2003-03-13
CURRENT FILING DATE: 2003-03-13
CURRENT FILING DATE: 2003-03-13
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PRIOR FILING DATE: 1998-08-07
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279.00
94.00%
92.00%
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MOLECULE TYPE: CDNA
FEATURE:
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; LOCATION: 16..255
US-09-759-584-48
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Best Local Similarity: 9
Query Match:
DB:
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166 AAGAATCAGTGCATTAACCTTGAGAAGCACGACATGATCTTGCAACTATGTCTTCCCA 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 AAGTTGTGCGAAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/10006252A
| Sequence 19, Application US/10006252A
| Publication No. US20020152498A1
| GENERAL INFORMATION:
| APPLICANT: De Samblanx, Genoveva
| APPLICANT: Rees, Sarah
| TITLE OF INVENTION: Antifungal Proteins
| TITLE OF INVENTION: Antifungal Proteins
| FILE REFERENCE: STN-034DV
| CURRENT APPLICATION NUMBER: US/10/006,252A
| CURRENT APPLICATION NUMBER: 09/077,951
| PRIOR APPLICATION NUMBER: 09/077,951
| PRIOR FILING DATE: 1996-06-10
| PRIOR FILING DATE: 1996-12-13
| PRIOR FILING DATE: 1996-12-13
| PRIOR FILING DATE: 1996-12-12
| NUMBER OF SEQ ID NOS: 77
| SEQ ID NOS: 77
| SEQ ID NOS: 77
| SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255
PRIOR APPLICATION NUMBER: PCT/GB96/03068
PRIOR FILING DATE: 1996-12-12
PRIOR APPLICATION NUMBER: GB 9606552.9
PRIOR PILIG DATE: 1996-03-28
PRIOR PILIG DATE: 1996-03-28
PRIOR PILIG DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 141
SEQ ID NO 45
LENGTH: 414
                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
Gaps:
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279.00
94.00%
92.00%
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279.00
94.00%
92.00%
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ORGANISM: Raphanus sativus
                                                                                                                                                                                                                   TYPE: DNA

) ORGANISM: Raphanus sativus

US-10-388-361A-45
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Best Local Similarity:
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Query Match:
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us-10-006-252a-10.rnpb

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Best Local Similarity:
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US-09-938-842A-2046
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166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATGTTTGCAACTATGTTCTCCCA 225
                                                    40
                                                    LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
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0 0
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: For PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                   Sequence 13, Application US/09732561
Sequence 13, Application US/09732561
Settle No. US20020035738A1
GENERAL INFORMATION:
APPLICANT: Terras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Razan, Kemal
APPLICANT: Razan, Kemal
APPLICANT: Brockaert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-006-252A-10 (1-50) x US-09-732-561-13 (1-403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 32,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                          226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                    41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA AG Products
STREET: 1800 Concord Pike
CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 403 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274.00
94.00%
90.00%
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Best Local Similarity:
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US-09-732-561-13
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Query Match:
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US-U9-9348-844A-2U46
) Sequence 2046, Application US/09938842A
) Sequence 2046, Application US/09938842A
) Patent No. US20020160378A1
) GENERAL INPORMATION:
APPLICANT: Harper, Joef
APPLICANT: Wang, Xun
APPLICANT: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2046

LENGTH: 243
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Publication No. US2000009476A9
CENERAL INFORMATION:
APPLICANT: HATPEY. Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
116 AAGTTGTGCGAGGCCAAGTGGGACATGGTCGGAGTTTGCGGAAACAGTAACGCGTGC 175
                                                                                               21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LysleuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys 20
                                                                     21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Arabidopsis thaliana
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94.00%
88.00%
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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                             1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                                                                                                                                             ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              us-09-732-561-15
; Sequence 15, Application US/09732561
; Patent No. US2002035738A1
; GENERAL INFORMATION:
APPLICANT: Terras, Franky
; APPLICANT: Penninckx, Iris
APPLICANT: Penninckx, Iris
APPLICANT: Razan, Kemal
APPLICANT: Razan, Kemal
TITLE OF INVENTION: Blant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPENDENCE ADDRESS:
ADBESSEE: ZENECA AG Products
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY.
                                                                                                                                                                                                                                                                                                                                                                                               US-10-006-252A-10 (1-50) x US-09-938-842A-2046 (1-243)
                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: S379
LENGTH: 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 GCACACAAGTGTATCTGTTACGTCCCATGT 240
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-UN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                           TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                          1.08e-29
272.00
94.00%
88.00%
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Best Local Similarity:
Query Match:
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US-09-732-561-15
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182 AAGAATCAGTGCATTAACCTTGAAGGAGCCAAACATGGATCATGCAACTATGTATCTTCCCA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 607, Application US/0989576
; Sequence 607, Application US/0989576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
    APPLICANT: Budworth, P.
    APPLICANT: Brown, D.
    APPLICANT: Chang, H.
    APPLICANT: Chang, H.
    APPLICANT: Promoters for regulation of plant expression:
    APPLICANT: Wang, X.
    APPLICANT: Wang, X.
    APPLICANT: Wang, X.
    APPLICANT: Wang, X.
    APPLICANT: Cooper, Bret
    TITLE OF INVENTION: Promoters for regulation of plant expression:
    TITLE OF INVENTION: December: US/09/887,576
    TITLE OF INVENTION: UNMBER: US/09/887,576
    PRIOR APPLICATION NUMBER: US 60/213,848
    PRIOR APPLICATION NUMBER: US 60/213,848
    PRIOR APPLICATION NUMBER: US 60/214,087
    PRIOR FILING DATE: 2000-06-23
    PRIOR FILING DATE: 2000-06-23
    PRIOR FILING DATE: 2000-12-29
    NUMBER: OF SEQ ID NOS: 875
    SOFTWARE: FeatSEQ for Windows Version 4.0
    SEQ ID NO 607
    LENGTH: NAME
                                                                                                                                                                                                                                                                                                                                                                                                                  4 4 W W O O
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Matches:
Conservative:
Mismatches:
Indels:
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NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 GCACACAAGTGTATCTGTTACGTCCCATGT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
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ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(400)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                     2.08e-29
                                                                                                                                                                                                                                                                                                                                                                                                                                         272.00
94.00%
88.00%
90.37%
                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
STRAIN: PDF1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-887-576-607
                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-887-576-607
                                                                                                                                                                                                                                                                                                                                             US-09-732-561-15
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Pred. No.: 2.08e-29 Length: 400
Score: 272.00 Matches: 44
Percent Similarity: 94.00$ Conservative: 3
Best Local Similarity: 96.00$ Mismatches: 3
Query Match: 90.37$ Indels: 0
DB: 05-10-006-252A-10 (1-50) x US-09-887-576-607 (1-400)
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model
Run on:
May 13, 2004, 10:53:23 ; Search time 2518 Seconds
(without alignments)
592.974 Million cell updates/sec
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Title:
Perfect score: 301
Sequence: 1 KLCERSSGTWSGVCGNNNAC......QHGSCNYVFPAHKCICYFPC 50
Scoring table: BLOSUM62
Xgapop 10:0, Xgapext 0.5
Ygapop 10:0, Ygapext 0.5
Fgapop 6:0, Fgapext 7:0
Delop 6:0, Delext 7:0
Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:\*

1: em\_estha:\*
2: em\_esthum:\*
3: em\_esthum:\*
4: em\_esthum:\*
5: em\_estpov:\*
6: em\_estpov:\*
7: em\_estpov:\*
10: gb\_est1:\*
10: gb\_est2:\*
11: gb\_est2:\*
11: gb\_est2:\*
12: gb\_est2:\*
13: gb\_est3:\*
14: em\_estfum:\*
15: em\_estfum:\*
16: em\_estfum:\*
17: em\_ests.
18: em\_gss\_fum:\*
18: em\_gss\_fum:\*
18: em\_gss\_fum:\*
22: em\_gss\_fum:\*
22: em\_gss\_fum:\*
23: em\_gss\_fum:\*
24: em\_gss\_fum:\*
25: em\_gss\_fus:\*
26: em\_gss\_fus:\*
27: em\_gss\_fus:\*
28: gb\_gssl:\*
28: gb\_gssl:\*

## 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	140 HC057	224 BN40	IRES BNAS	3613 BN40	3047 BN40.	1226 BN40.	1995 BN45.	3784 BN45.	1092 BN45.(	3924 BN45.	3627 BN45.0	3661 BN45.	3840 BN40.	1628 BN40.	7429 BN40.	129 BOMSG	3938 BN45.	9085 BN40.0	3779 BN45.	1090 BN45.	625 BN40.	1168 BN45.0	3944 BN45.	491 BNZ5.C	977 BN45.	1983 BN45.0	7413 BN25.C	.294 BN40.0	.479 BN40.0	1068 BN45.C	592 BN40.0	611 BN45.0	O THE BUTO	008 BN45.	680 BN40	332 BN25.0	014 BN40.04	1392 BOGWE36	491 odd80q0	0831392	.57 32717 La	316118 AV81611	
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## ALIGNMENTS

RESULT 1

CA992140

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DEFINITION HC0577 GIBCOBRL CAT. NO. 19643-014 Brassica rapa subsp. pekinensis

CA992140

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CD834852.1 GI:32516792
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E 1 (bases 1 to 346)
S Gao.R.J., Dai, D.P. and Ma.R.C.
Expressed sequence tags of heading leaf during the heading process of Chinese cabbage
Orpublished (2003)
Contact: Rongaci, Ma
Plant Functional Genomics
Beijing AgroBiotechnology Research Center
Haidian District, Ban-Jing Rd., Beijing 100089, China
Tel: 86 10 5150 3980
Email: rcmal@yahoo.com
Seq primer: T7
High quality sequence stop: 346
POLYA-No.
                                                                                                                                                                                                                                                    / Corganism="Brassica rapa subsp. pekinensis"
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Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
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Brassica napus
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CD834852
BN45.043G08F011229 BN45 Brassica napus CDNA clone BN45043G08, mRNA
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Brassica napus
Brassica napus
Brassica napus
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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93, Tue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr).

Location/Qualifiers
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Matches:
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Definition of the framework of the frence 13.3 1 69 47 54 00

Fax: 33 1 69 47 54 10

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

Location/Qualifiers

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                                                                                                                                          CD833047 449 bp mRNA linear EST 10-JUL-2003 BN40.065M05F011229 BN40 Brassica napus cDNA clone BN40065M05, mRNA sequence.
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457 bp mRNA linear BST 10-JUL-2003

HA40.058310F011019 BN40 Brassica napus cDNA clone BN40058J10, mRNA sequence.
CD831226

CD831226.1 GI:32513166

EST.
    Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 449)
Genoplante.
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Contact: Genoplante
Genoplante
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EST.
Brassica napus (rape)
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CD833047
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                                                                                                                                                  Brassica napus
Brassica napus
Brassica napus
Brassica napus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 427)
Genoplante.
Genoplante a major partnership french program in plant genomics
Umpublished (2003)
Contact: Genoplante
Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://genoplante.com and http://genoplante-info.infobiogen.fr).
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CD833613.1 GI:32515553
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94.00%
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SOURCE

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CD833784 476 bp mRNA linear EST 10-JUL-2003 BN45.001122F010914 BN45 Brassica napus cDNA clone BN45011122, mRNA
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plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Contact: Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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clone="BN45001122"

/tissue type="seed"

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  Brassica napus (rape)
Brassica napus
Brassica napus
Bukaryota; Viribiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                Genoplante, a major partnership french program in plant genomics Unpublished (2003)
                                                                                                                                                                                                    Party Herri Rochefort 91025 EVRY CEDEX France 93, true Herri Rochefort 91025 EVRY CEDEX France Fax: 33 1 69 47 54 00 Fax: 33 1 69 47 54 10 Fiss sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
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                                                                                                                                                                                                                                                                                                                                                        /organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
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Brassica napus
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
[ Dases 1 to 476]
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Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
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Tel: 33 1 69 47 54 00
Fax: 31 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                       1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                          160 AAGTIGIGGGGGGCAAGTGGGACATGGTCAGGAGTTTGTGGAAACAATAATGCGTGT
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747
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Matches:
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/db_xref="taxon:3708"
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                                                                                                                                                                                                                            280 GCTCACAAGTGTATCTGCTATTTCCCTTGT 309
                                                                                                                                                                                                            41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                           US-10-006-252A-10 (1-50) x CD833784 (1-476)
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EST.
Brassica napus (rape)
Brassica napus
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284.00
96.00%
94.00%
284.00
96.00%
94.00%
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Best Local Similarity:
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DB:
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CD834092
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## 481 bp mRNA linear EST 10-JUL-2003
BN45.040A03F011018 BN45 Brassica napus cDNA clone BN45040A03, mRNA
sequence.
CD833924
CD833924.1 GI:32515864
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                                                                                                                                                                                                 Brassica napus (rape)
Brassica napus
Brassica napus
Brassica napus
Brassica napus
Brassica napus
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Trachighyta; Magnoliophyta; eudicotyledons; core eudicots;
I (bases I to 481)
Genoplante.
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
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Contact: Genoplante Genoplante Genoplante
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1 1 2 0 0 0
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Matches:
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/clone="BM4504030"
/tissue_type="seed"
/clone_lib="BM45"
41 AlaHisLysCysIleCysTyrPheProCys 50
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CD833627.1 GI:32515567
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Brassica napus
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Best Local Similarity: 5
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CD833924
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KEYWORDS
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CD833627
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/nol type="mRNA"
/ulfivar="Jet neuf"
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/tissue_type="seed"
/clone_lib="BNA5"
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Matches:
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     Location/Qualifiers
1. .523
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CD828840.1 GI:32510780
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Brassica napus
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BN45.001C04F010914 BN45 Brassica napus cDNA clone BN45001C04, mRNA
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1 (bases 1 to 523)
Genoplante
Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 482)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                General Berri Rochefort 91025 EVRY CEDEX France
721: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
                                                                                                                                                  93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                         Genoplante.
Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                               482
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                   1. .482
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/culTivar="Jet neuf"
/db xref="taxon:3708"
/clone="RN45001A11"
/tissue type="seed"
/clone_Tib="BN45"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 GCTCACAAGTGTATCTGCTATTTCCCTTGT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
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284.00
96.00%
94.00%
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Brassica napus
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Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
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VERSION
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
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CD628840
BN40.040A23F011019 BN40 Brassica napus CDNA clone BN40040A23, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 543)
Genoplante.
                                                                                                                                                                                                                                     93, run Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
                                                                                                                                                               1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
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Length:
Matches:
Conservative:
Mismatches:
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261
                                 RESULT 15
CD829429
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                  CUBJ0628 543 bp mRNA linear EST 10-JUL-2003
BN40.046D16F011221 BN40 Brassica napus CDNA clone BN40046D16, mRNA
Sequence.
                                                               201 AAGAATCAGTGCATTCGACTAGAGAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPheFro 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                93, rue Henri Rochefort 91025 BVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Mismatches:
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Matches:
                                                                                                                                                       41 AlaHisLysCysIleCysTyrPheProCys 50
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                      Gaps:
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                                           US-10-006-252A-10 (1-50) x CD828840 (1-543)
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                                                                                                                                                                                                                                                            CD830628
CD830628.1 GI:32512568
                                                                                                                                                                                                                                                                                            Brassica napus (rape)
Brassica napus
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284.00
96.00%
94.00%
94.00%
94.35%
Best Local Similarity:
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Best Local Similarity:
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CD829429

CD829429

ANA0.042B06F011226 BN40 Brassica napus CDNA clone BN40042B06, mRNA Sequence.
CD829429
                                                                                                                                                         CD82929.1 GI:32511369
EST.
Brassica napus (rape)
Brassica napus
Brassica napus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots, rosids, eurosids II; Brassicales; Brassicaceae, Brassica.
1 (bases 1 to 646)
Genoplante.
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                                                                                                                                                                                                                                                                                                                      Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
                                                                                                                                                                                                                                                                                                                                                                                         93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
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Matches:
Conservative:
Mismatches:
Indels:
                      290
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/organism="Brassica napus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 AlaHisLysCysIleCysTyrPheProCys 50
255 GCTCACAGAGGCATCTGCTACTTCCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mol type="mRNA"

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/tissue type="seed"
/clone_lib="BN40"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: May 13, 2004, 12:18:04 Job time: 2525 secs
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284.00
96.00%
94.00%
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Best Local Similarity:
Query Match:
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Pred. No.:
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Perfect score:

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Scoring table: Sequence:

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                      Abp53725
Aaw40351
Abp81292
Aay57265
Abp53726
Abp53726
Abm40345
Aaw40345
Aaw40345
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Aaw40349
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Aab20220
Aab49470
Aab61793
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Aay70323
Aay84058
Aaw26372
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Aay84067
Aaw19281
Aaw19616
Aaw26375
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Aae10625
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                                                                                                                             AAG41694
AAW40349
AAY00738
AAB67417
AAB20220
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AAW40347
AAY3033
AAY4058
AAW26372
AAW26374
AAW26371
AAW46066
AAY84066
AAY84066
           AAY57564
ABP53725
AAW40351
                                                                   AAY57565
ABP53726
AAW40345
AAB61794
AAW35560
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AAW26375
AAY00737
                                            AAW40346
ABP81292
                                                                                                                                                                                                  AAB61793
AAY84060
                                                                                                                                                                                      AAB49470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR33706 standard; protein; 80 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antifungal protein Rs-AFP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
Raphanus sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9305153-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
07-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1993.
AAR33706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
Aar33706 Antifunga
Aav7325 Antimicro
Aaw19280 Raphanus
Aaw13617 Radish an
Aar33708 Antifunga
Aar57327 Antimicro
Adc31222 Brassica
Adc31224 Brassica
Aay91117 Raphanus
Aay91117 Raphanus
                                                                          May 11, 2004, 16:57:25 ; Search time 59.5 Seconds (without alignments) 3931.922 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                  OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                             1586107 seqs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                    0.5
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AAR57325
AAW19510
AAW33708
AAR57327
ADC51222
ADC512224
AAY911117
AAY911117
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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2: geneseqp1980s:*
2: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
5: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2003bs:*
                                                                                                                         US-10-006-252A-19
752
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Maximum DB seq length: 2000000000
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Terras FRG;

SB, Rees

Osborn RW,

BPA,

Cammue

Vanderleyden J; Broekaert WF,

80 80 80 80 80 80 80

Length

Query

Result Š.

Database

WPI; 1993-100978/12.

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136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                             This sequence is antifungal protein Rs-AFP1 from Raphanus sativus. The exact source and isolation of the encoding DNA sequence is unclear from the specification. The protein is useful for combating fungi or bacteria eg gram positive bacteria and plant pathogenic fungii. It has moderate sensitivity to ions and an apparent low toxicity for cultured human cells. Plants transformed with the encoding DNA show increased disease resistance. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                          1 PheGlualaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCys1leAsnLeuGluLysAla 60
Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                                                                                                                                                                 76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                           ATGGCTAAGTTTGCGTCCATCATCGCTCTTTTTGCTGCTCTTTTTTGCTGCT
                                                                                                                                                                                                                                   880000
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                       Gaps:
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                                                      Disclosure, Fig 35; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR57325 standard; protein; 80 AA
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N-PSDB; AAQ70128.
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                                                                                                                                                                                                                                                                               Similarity:
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                                                                                                                                                                                             Sequence 80 AA;
                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JAN-1994;
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14-FEB-1995
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Query Match:
DB:
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                                                               plant-derived antimicrobial proteins are expressed in endosymbiotic clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFPI from R. sativus. The full-length cDNA sequence of Rs-AFPI is given in AAQ70128, and the amino acid sequence predicted from this sequence in AAR57325. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antifungal protein, candida, fungal resistance, food additive, radish, crop protection; plant defensin, bacterial protection, preservative.
                                                                                                                                                                                                                                                                                                                                                                                           76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                             21 PheGludlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGLyThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                         196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                  880000
                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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13. .80
/label= antifungal_protein_1
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                                                                                                                                                                                                                                                         Gaps:
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                                              Disclosure; Page 32; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW19280 standard; protein; 80
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96GB-00006552.
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100.00%
100.00%
58.78%
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(first entry)
                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                        correct PN field.)
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                                                                                                                                                                 Sequence 80 AA;
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28-MAR-1996;
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19-JAN-1998
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                                                                                                                            Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.
                                                                                                                                                                                                      This protein sequence is a Raphanus sativus (radish) antifungal protein also been produced (see AAM12282-92, AAM19294-98, AAM19201-04, AAW19330-34 and AAW31765-83). Plants containing DMs sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease tolerance of crops, either pre or post harvest. Festsance or disease tolerance of crops, either pre or post harvest. When applied to plants they may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorganism capable of expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct Plifield.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TICGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTGAAGTGTATCTGCTTTCCTTGT 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sijtsma L, Van Amerongen A;
Borremans FAM, Rees SB;
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Matches:
Conservative:
Mismatches:
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                                     Puijk WC, Schaaper WMM,
, Samblanx GW, Fant F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Radish antifungal protein 1 (Rs-AFP1)
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                                                                                                                                                                               Claim 1; Fig 2; 65pp; English.
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434.00
98.75%
98.75%
57.71%
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                                                                                        1997-332786/30.
           (ZENE ) ZENECA LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
                                                                                                    N-PSDB; AAT72333
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                                                               Van Gelder WMJ;
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 80 AA;
                          Meloen RH, Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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This polypeptide comrpsies the preprotein for radish antifungal protein I (Rs-APP1). Novel antifungal proteins are based on Rs-AFP1, Rs-AFP2 (see AAM19466), Rs-APP3 and Rs-AFP4, especially those in which Gly9 is repaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by Met. Mutants (see AAW26371-90) of Rs-AFP2 are specifically claimed. The mutants show improved salt tolerant antifungal activity, particularly
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                                                                                                                                                                                                                                                                                                                                                                                                                                       New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents.
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Mismatches:
Indels:
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Matches:
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Location/Qualifiers
1. .29
/label= Pro-peptide
                                                                                    30. .80
/label= Mat_protein
/note= "RSAFP1"
                                                                     'note= "encoded by
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434.00
98.75%
98.75%
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(first entry)
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                                                                                                                                                                                                                                                                                                          (ZENE ) ZENECA LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 80 AA;
                                                                                                                                                                                                                                                                                                                                                   Broekaert WF,
                                                                                                                                                                                                                                                                         13-DEC-1995;
                                                                                                                                                                                                                                       12-DEC-1996;
                                                                                                                                                               WO9721814-A1
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07-JUL-1993
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Key
Peptide
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196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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                                                                                                                                                                                                                                                                                                                                                                                                 Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is part of antifungal protein Rs-AFP2, decoded from a mutaganised RsAFP1 clone derived from Raphanus sativus. The protein is useful for combating fungi or bacteria eg gram positive bacteria and plant pathogenic fungii. It has moderate sensitivity to ions and an apparent low roxicity for cultured human cells. Plants transformed with the encoding DNA show increased disease resistance. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG
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                                         Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                                                                                                                                                                                                                                                                                                                       Cammue BPA, Osborn RW, Rees SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
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92GB-00013526.
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433.00
98.75%
97.50%
57.58%
              Antifungal protein Rs-AFP2.
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-100978/12.
                                                                                                       Raphanus sativus.
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                                                                                                                                                                                                                                                                                                                                     Vanderleyden J;
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                                                                                                                                   W09305153-A1
                                                                                                                                                                                                27-AUG-1992;
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Pred. No.:
                                                                                                                                                                                                                                                           25-JUN-1992;
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DB:
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AC AARS
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СD
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Antimicrobial, Rs-AFP2; symbiosis; disease-resistance; fungus-resistance;
Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte;
PCR; polymerase chain reaction; mutagenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgFroSerGlyThrTrp 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial protein producing endo-symbiotic microorganisms - is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 33-34; 39pp; English.
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433.00
98.75%
97.50%
                                                                  (first entry)
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                                 (revised)
                                                                                                                                    Antimicrobial Rs-AFP2
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                                                                                                                                                                                                                                                                                                                                              Raphanus sativus.
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                                 25-MAR-2003
                                                                  14~FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to disease caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present amino acid sequence represents a Brassica defensin protein of the invention.
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MetalaiyspheValSerileileAlaieuleuPheAlaAlaieuValleuPheAlaAla
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                                                                                                                                                                                                                                                                                                                        (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                         Brassica oleracea defensin protein.
                                                                                                                               seedling damping-off disease; filam
sheath blight disease; leaf blight.
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                             (first entry)
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97.50%
97.50%
57.45%
                                                                                                                                                                                                                                                                                                                                                       2003-621123/59
                                                                                                                                                                           Brassica oleracea
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Best Local Similarity:
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N-PSDB; ADC51221.
                                                                                                                                                                                                       JP2003088379-A.
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                             18-DEC-2003
                                                                                                                                                                                                                                      25-MAR-2003
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ADC51222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
ADC51224
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Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to disease retained by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, such as: rice white leaf blight, brownstripe diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present amino acid sequence represents a Brassica defensin protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 PheGludlaProThrMetValGludlaGlnLysLeuCysGludrgProSerGlyThrTrp
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                                                                                                                                                                                                                              composite disease resistance; pathogenic bacteria; rice white leaf blight; brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight.
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                                                                                                                                                                                                   antimicrobial protein; defensin; transgenic plant;
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Mismatches:
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Matches:
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       80
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ADC51224 standard; protein;
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425.00
96.25%
96.25%
56.52%
                                                                                                    (first entry)
                                                                                                                                                    Brassica defensin protein.
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N-PSDB; ADC51223.
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Best Local Similarity:
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                                                                                                    18-DEC-2003
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                                                  ADC51224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
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No.:
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03-JUL-2000 (first entry)

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TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated DNA from Raphanus sativus used to transform a microbe and a plant to produce an antibacterial protein used to increase resistance of rice paddy against pathogenic microbes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 PheGluhlaProThrMetValGluhlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents an antibacterial protein, designated radishin, isolated from Raphanus sativus (radish). A phage or plasmid comprising radishin can be used for increasing resistance of paddy and rice blast disease against pathogenic microbes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 ATGGCTAAGTTTGCGTCCATCATCGCCTCTTTTTGCTGCTCTTGTTCTTTTGCTGCT
                                                                                                                                                         Raphanus sativus; antibacterial; plant; resistance; paddy; radishin; pathogenic microbe; radish; rice blast disease.
                                                                                                                            Raphanus sativus antibacterial protein radishin SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY84072 standard; protein; 187 AA.
                                 AAY91117 standard; protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 4-5; 7pp; Japanese.
                                                                                                                                                                                                                                                                                                 98JP-00288472
                                                                                                                                                                                                                                                                                                                               98JP-00288472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.04e-38
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423.00
97.50%
93.75%
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                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-389821/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                       Raphanus sativus.
                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA53190.
                                                                                                                                                                                                                                     JP2000116379-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 80 AA;
                                                                                                                                                                                                                                                                                                 09-OCT-1998;
                                                                                                                                                                                                                                                                                                                             09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                              06-OCT-2000
                                                                                                                                                                                                                                                                 25-APR-2000.
                                                                AAY91117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
DB:
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RESULT 9
AAY91117
ID AAY91
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The present sequence represents a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) 1 and the antifungal protein 2 (RSAPP2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is posttranslationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, v. S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGAACATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                           Antimicrobial protein; AMP1, transgenic plant, linker propeptide; protein expression; plant defensin; RsAFP2; antifungal protein; AFP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ray JA;
                           Amino acid sequence of a fusion protein of DmAMP1 and RSAFP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      De Bolle MFC, Evans IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
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                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 33; Fig 34; 151pp; English.
                                                                                                                                                                                                       "DMAMP1"
                                                                                                                                                                                                                                      /note= "linker"
                                                                                                                                                                                                                                                                         /note= "RsAFP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Broekaert WF, Francois IEJA,
                                                                                                                                                                                                                                                                                                                                                                      99WO-GB002716.
                                                                                                                                                                                                                                                                                                                                                                                                    98GB-00018001.
98GB-00026753.
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96.25%
95.00%
55.59%
                                                                                                                                                                                                                                                          .187
                                                                                                                                                                                                                        79. .136
                                                                                                                                                                                           29. .78 /note= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZENE ) ZENECA LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
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N-PSDB; AAZ99339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 187 AA;
                                                                                                                        Dahlia merckii.
Unidentified.
                                                                                                                                                                                                                                                                                                       WO200011175-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                      17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                      18-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                     02-MAR-2000
                                                                                                          Synthetic.
                                                                                                                                                                                           Protein
                                                                                                                                                                                                                        Peptide
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TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG 135

75 20

ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTTGCTGCT

4 4 4 0 0

Conservative: Mismatches: Indels: Gaps:

417.00 95.00% 92.50% 55.45%

Matches:

195

40

255

ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

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(first entry) (revised)

CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT

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1 MetAlaLysPheAlaSerIleIleValLeuLeuPheValAlaLaLeuValValPheAlaAla
                                                                                                                                                                                                                                                                                                                 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wasabia japonica antibacterial protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wasabia japonica; antibacterial; food additive.
                                                                                                                       US-10-006-252A-19 (1-414) x AAB61792 (1-80)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY57564 standard; protein; 80
                               Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP11313678-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2003
01-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY57564;
                                                                                                                                                                                                                                         94
                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                             196
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                                                                     Query Match:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to sunflower anti-pathogenic proteins such as pathogenesis-related protein-5 (PR5), defensin and berberine bridge enzyme (BBE). DNA constructs containing nucleotide sequences encoding the anti-pathogenic proteins are useful for increasing resistance against pathogens e.g. fungal pathogen in moncot or dicot plants. The purified sunflower proteins (PR5, defensin or BBE) and compositions containing the proteins are useful for controlling plant pathogen by using procedures of spraying, dusting, scattering or seed coating, to the plants or the proteins are useful for controlling plant pathogen by using procedures of spraying, dusting, scattering or seed coating, to the plants or the proving are useful as genetic markers in disease resistance breeding programs. Promoters capable of driving expression of the proteins are useful as grenting proteins and insert resistance genes. The proteins can also be used in agricultural and pharmaceutical compositions as antifungal and antimicrobial agents. The nucleotide sequences encoding and for enhancing plant defense mechanism. The present sequence conservance represents a radish antifungal defensin (Swiss-Prot Accn No. P30230),
                                                                                                                       255
128 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerArgThrTrp 147
                                                                                                                                     Increasing pathogen (e.g. fungus, bacteria and virus) resistance in plants, comprises transforming plants with a DNA construct containing a nucleic acid sequence encoding anti-pathogenic proteins.
                                                                                                                                                                                                                                                                                                                                                                             Sunflower; anti-pathogenic; pathogenesis-related protein-5; PR5; BBE; defensin; berberine bridge enzyme; plant pathogen; disease resistance; agricultural; pharmaceutical; antifungal; antibacterial; antiviral; antimicrobial; gene therapy; radish.
                                   136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
                                                           CGACATGGAICTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Γυ G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hu X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duvick JP,
                                                                                                                                                                                                                                   Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 4; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIONEER HI-BRED INT INC. CURAGEN CORP.
                                                                                                                                                                                                                             AAB61792 standard; protein; 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0140646P.
99US-0162904P.
2000US-00589733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUN-2000; 2000WO-US017090
                                                                                                                                                                                                                                                                                                                                           Radish antifungal defensin.
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bidney DL, Crasta OR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-102729/11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raphanus sativus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200078983-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUN-2000;
                                                                                                                                                                                                                                                                                                       20-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999
                                                                                                               196
                                                                                                                                                   168
                                                                                                                                                                                                                                                                 AAB61792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PION-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURA-)
                                                                                                                                                                                         RESULT
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The present sequence represents an antibacterial protein isolated from Wasabia japonica. The antibacterial protein can be used as a food or feed additive. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                           An antibacterial protein gene of Wasabia japonica - useful as a food- or feed-additive.
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                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                  Length:
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                                                                                                                                                                                                               Claim 1; Page 13; 16pp; Japanese.
98JP-00121303
                                  98JP-00121303
                                                                                                                                                                                                                                                                                                                                                                           2.98e-36
407.00
96.25%
90.00%
54.12%
                                                                                                        WPI; 2000-057353/05.
                                                                    (IWAT-) IWATE KEN.
                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                       N-PSDB; AAZ39123.
                                                                                                                                                                                                                                                                                                                           Seguence 80 AA;
                                  30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
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80

Alignment Scores: Pred. No.:

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136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGÇA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 TICGAAGCACCAACAAIGGIGGAAGCACAGAAGTIGIGCGAAAAGCCCAAGIGGGACAIGG 135
                                                                                                                                                                     61 ArgHisGlySerCysAsnTyrIlePheProTyrHisArgCysIleCysTyrPheProCys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents an Arabidopsis PDF1.2 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensing gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
  21 PheGluAlaProSerMetValGluAlaGlnLysLeuCysGluLysSerSerGlyThrTrp 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetalaLysPheAlaSerIleIleThrLeuIlePheAlaAlaLeuVheAhaAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Manners JM;
                                                                        196 CGACATGGATCTTGCAACTATGTCTTCCCAGCACAAGTGTATCTGCTACTTCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 ATGCCTAAGTITGCGTCCATCATCGCACTICTTTTGCTGCTGCTTGTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras FRG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
71
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-006-252A-19 (1-414) x AAW40351 (1-80)
                                                                                                                                                                                                                                                                                         AAW40351 standard; protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Fig 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-GB001672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96GB-00013753.
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403.00
95.00%
88.75%
53.59%
                                                                                                                                                                                                                                                                                                                                                                                                                                 A. thaliana PDF1.2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a disease-resistant plant in which a wasabi gamma-thionin gene is introduced. Also described is a method for the creation of the above disease-resistant plant by introducing a wasabi gamma-thionin gene to a plant. The present sequence represents a Butrema wasabi (Wasabia japonica) gamma-thionin protein from the present
                                                                                               TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
                                                                                                                                                                                            TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                         CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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                         1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuVheSerAla 20
                                                                                                                      9
                                                                                                                                                                                                                                                                                                                   ArgHisGlySerCysAsnTyrllePheProTyrHisArgCysIleCysTyrPheProCys 80
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                                                                                                                                                                                                                      41 SerGlyValCysGlyAsnAsnAsnAsnAshAcysEysAsnGlnCysIleAsnLeuGluGlyAla
ATGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wasabia japonica; gamma-thionin; plant; disease-resistant plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A disease-resistant plant in which wasabi gamma-thionin gene is introduced, creation of the disease-resistant plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wasabía japonica gamma-thíonín proteín SEQ ID NO:2.
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP53725 standard; protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 8; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAR-2001; 2001JP-00083526.
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Best Local Similarity:
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           80
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 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
                                         CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTGT
                                                     61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys
                                                                                                                                                                                                                                                                                                                                                                                                                              Manners JM;
                                                                                                                                                                                       Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;
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Conservative:
Mismatches:
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/label= signal
30. .80
/label= PPD1.2
/note= "plant defensin"
                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 1; 72pp, English.
                                                                                                      AAW40346 standard; protein; 80
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                                                                                                                                                                   A. thaliana PDF1.2 protein.
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                                                                                                                                                                                                                       Arabidopsis thaliana.
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N-PSDB; AAV10633.
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                                        196
                                                                                                                           AAW40346;
                                                                                                                                                                                                                                                     Peptide
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16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTTGCTGCT 75

US-10-006-252A-19 (1-414) x AAW40346 (1-80)

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Best Local Similarity:

Query Match: DB:

Percent Similarity:

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135
                                                                                                                                                  136 TCAGGAGICTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                  GGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
40
                                                                                                                                                                        41 SerGlyValCysGlyAsnSerAsnalaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
                                                                                                                                                                                                                                                          TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG
                                                                                        21 PheAspAlaProAlaMetValGluAlaGlnLySLeuCysGluLysProSerGlyThrTrp
                                                                                                                                                                                                                                                                                                                                          Search completed: May 11, 2004, 17:02:15 Job time : 62.5 secs
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119, Appl

18, Appl

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
FILING DATE:
CLASSIFICATION NUMBER: US/08/377,687
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/002,480
FILING DATE: 04-JAN-1993
ATTONEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
US-09-929-381D-15
US-08-377-687-19
US-08-377-687-19
US-08-777-192-19
US-08-777-192-19
US-08-777-192-19
US-08-777-192-19
US-09-077-948A-34
US-09-077-948A-34
US-09-077-948A-34
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US-09-077-951-58
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US-09-077-951-28
US-09-077-951-41
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APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: WANDERLENDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
CCONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-377-687-49
; Sequence 49, Application US/08377687
; Patent No. 5538525
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   RESULT
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-MODEL=frame+ n2p.mcdel -DEV=xlp
-DEV
-DEV=xlp
-DEV
-DEV=xlp
-DEV=xl
                                                                                                                                                                                                                                 (without alignments)
1943.014 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 49,
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                                                                                                                                                                                           May 11, 2004, 17:00:09 ; Search time 22 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ued_Patents_AA:*
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                           OM nucleic - protein search, using frame_plus_n2p model
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US-08-777-192-49
US-08-971-982-49
US-09-103-489-20
US-09-829-381D-20
US-09-829-381D-20
US-08-377-687-59
US-08-777-982-59
US-08-971-982-59
US-09-971-982-59
US-09-689-733C-21
US-09-689-733C-21
US-08-677-706-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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752
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seq length: 200000000
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Match Length DB
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Sequence:
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Maximum DB s
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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
FLING DATE:
CLASSIFTCATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                           880000
                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
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REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
                                                                                                                                                                                                                                                                                                                                                                                   US-10-006-252A-19 (1-414) x US-08-377-687-49 (1-80)
                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUN D.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : CUSHMAN DARBY & CUSHMAN 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 49, Application US/0877192; Patent No. 5824869; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
               TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                        442.00
100.00%
100.00%
58.78%
                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-377-687-49
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Best Local Similarity:
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STREET: 110
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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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                                                                                                                                                                                                                                                                                                                                            21 PheGluAlaProThrMetValGluAlaGlnLySLeuCysGluArgProSerGlyThrTrp 40
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REGISTRATION NUMBER: 16,773
REPERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
                                                                                                                                                                                       880000
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Mismatches:
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CAMMUE, BRUNO P.A.
OSBORN, RUPERT W.
RRES, SARAH B.
TERRAS, FRANKY R.G.
VANDERLEXPEN, JOZZE
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                   Length:
Matches:
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                                                                                                                                                                                                                                              Indels:
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Patent No. 6187904
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
           TELEPHONE: 202-861-3000
TELEFAK: 202-822-0944
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-777-192-49
                                                                                                                                                                                               442.00
100.00%
100.00%
58.78%
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US-08-971-982-49
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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG 135
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Sequence 20, Application US/09103489

Patent No. 6215648

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Mah, Yonnie S.

APPLICANT: Rosenberger. Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSES: Charles E. Cohen, Monsanto Company, BB4F

STREET: 100 Chesterfield Village Parkway No. 6215048th

CITY: St. Louis

STARES: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Petentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/103,489 FILING DATE: 24-UUN-1998 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: CLASSIFICATION UNMERE: 34,565 RECERRENCE/DOCKET NUMBER: 34,565 REFERENCE/DOCKET NUMBER: 34,565 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFAX: (314) 537-6224 TELEFAX: (314) 537-6224
                                                                                                                                                                                                                                                                                   880000
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                   Length:
Matches:
                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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442.00
100.00%
100.00%
58.78%
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                                                                                                                                 TYPE: amino acid
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonkie S.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for ColTITLE OF INVENTION: Plant Pathogenic Fungi
FILE BYENERNCE: 38-21 (10700) C.
CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetalaLysPhealaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
                                                                                                                                                                                                                                                                                                                                                                                             1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
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Mismatches:
Indels:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                               US-10-006-252A-19 (1-414) x US-09-103-489-20 (1-80)
                                                                                                                                                                                             Length:
Matches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 20, Application US/09829381D; Patent No. 6653280; GENERAL INFORMATION:
                                                                                                                                                                                     4.74e-44
434.00
98.75$
98.75$
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434.00
98.75%
98.75%
57.71%
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Raphanus sativus
                                                                      STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-103-489-20
                                                         amino acid
                                                                                                                                                                                                                                                     Best Local Similarity:
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Best Local Similarity:
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US-09-829-381D-20
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Pred. No.:
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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135

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196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTCCTACTTTCCTTGT 255
76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
                                                                                   136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                       21 PheGluAlaGluThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
                                                                                                            41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 AIGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTTTTTGCTGCT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                   Sequence 59, Application US/08377687; Patent No. 5538525; GENERAL INFORMATION: APPLICANT: APPLICANT: CAMMUE, BRUND P.A. APPLICANT: CAMMUE, BRUND P.A. APPLICANT: OSDON, RUPERT W. APPLICANT: TERRAS, FRANKY R.G. APPLICANT: VANDERLEYDEN, JOZEF TILLE OF INVENTION: BIOCIDAL PROTEINS NUMBER OF SEQUENCES: 59 CORRESPONDENCE ADDRESS: CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CHIY: MACHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 59: SEQUENCE CHARACTERISTICS: LENGTH: 80 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433.00
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57.58%
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Best Local Similarity:
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136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                       196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
21 PheGluhlaproThrMetValGluhlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
                                                                              41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
                                                                                                                                                               61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTR:
ZIP: 20005
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
^^OPERATING SYSTEM: Patentin Release #1.0, Version #1.25
-^^OPERATING NOTE: Patentin Release #1.0, Version #1.25
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Mismatches:
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                                                                                                                                                                                                                                                                                                                        APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSDRON, RUBERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/ACENT INFORMATION:
NAME: NOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.3
TELEPHONE: 202-861-3000
TELEPAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                ; Sequence 59, Application US/08777192; Patent No. 5824869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-822-0343
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
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97.50%
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MOLECULE TYPE: protein
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Best Local Similarity:
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COUNTRY: USA
                                                                                                                                                                                                                                              US-08-777-192-59
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TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCCAAGTGGGACATGG 135
                                                                                                       136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAAGCA 195
                                                      21 PheGludlaProThrMetValGludlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
                                                                                                                                   41 SerGlyValCysGlyAsnAsnAsnAnaCysLysAsnGlnCysIleArgLeuGluLysAla
                                                                                                                                                                                 196 GGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTTCTTCTTGT
                                                                                                                                                                                                     61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys
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                                                                                                                                                                                                                                                                                      Sequence 21, Application US/09589733C

SEPTICANT: Davick, Jon

APPLICANT: Davick, Jon

APPLICANT: Davick, Jon

TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and

TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and

TITLE OF INVENTION: Genes and their Uses

FILE REFERENCE: 5118-90

CURRENT APPLICATION NUMBER: 05/09/646

PRIOR APPLICATION NUMBER: 60/140,646

PRIOR APPLICATION NUMBER: 60/162,904

PRIOR APPLICATION NUMBER: 60/162,904

PRIOR FILING DATE: 1999-11-01

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 21

LENGTH: 80
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Mismatches:
Indels:
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Matches:
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Sequence 23, Application US/09589733C
Patent No. 6677503
SENERAL INPORMATION:
APPLICANT: Bidney, Dennis L.
APPLICANT: Crasta, Oswald R.
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417.00
95.00%
92.50%
55.45%
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; ORGANISM: Raphanus sativus
US-09-569-733C-21
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                            RESULT 9
US_09-589-733C-21
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Pred. No.:
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TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGCCCAAGTGGACATGG 135
                                                                                    195
                                                                                                                                                   CGACATGGATCTTGCAACTATGTCTTCCCAGCTCAAGTGTATCTGCTACTTTCCTTGT 255
                    41 SerGlyValCysGlyAsnAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
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                                                                          TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,982
FILING DATE: 17-No. 6187904-1997
CLASSIFICATION: <UNknown>
PRIOR APPLICATION: <UNknown>
PRIOR APPLICATION NUMBER: US/08/02,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
RECIESTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                   REES, SARAH B.
TERRAS, FRANKY R.G.
VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
08-08-971-982-59
                                                                                                                                                                                                                                                                                                                       APPLICANT: BROEKAERT, WILLEM F. CAMMUE, BRUNO P.A. OSBORN, RUPERT W.
                                                                                                                                                                                                                          RESULT 8
US-08-971-982-59
'Sequence 59, Application US/08971982
'Patent No. 6187904
'Patent No. 6187904
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 202-861-3000
TELEFAX: 202-862-0944
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 80 amino acids
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98.75%
97.50%
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Percent Similarity:
Best Local Similarity:
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DB:
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76 ITCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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                                                                                                                                                                                     41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAala 60
                                                                                                                                                                                                                                                                                          61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
                                                                           21 PheGluGluProThrMetValGluAlaGlnLySieuCysGlnArgProSerGlyThrTrp
                                                                                                                                                 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
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APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wo, Yomie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCEs. 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F SITRET: 700 Chesterfield Village Parkway No. 5773696th CITY: St. Louis
APPLICANT: Duvick, Jon
APPLICANT: Hu, Xu,
APPLICANT: Hu, Xu,
APPLICANT: Lu, Guihua
TITLE OF INVENTION: Suuflower Anti-Pathogenic Proteins and
TITLE OF INVENTION: Genes and their Uses
FILE REFREENCE: 5718-06
CURRENT APPLICATION NUMBER: US/09/589,733C
CURRENT FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: 60/140,646
PRIOR APPLICATION NUMBER: 60/140,646
PRIOR APPLICATION NUMBER: 60/162,904
PRIOR FILING DATE: 1999-10-1
NUMBER OF SEQ ID NOS: 41
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-627-706-15; Sequence 15, Application US/08627706; Patent No. 5773696; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.38e-39
397.00
92.50%
87.50%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Arak
US-09-589-733C-23
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DB:
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76 TICGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCAAGTGTATCTGCTACTTTCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 PheGluhlaProThrMetValAspAla---ArgLeuCysGluhrgProSerGlyThrTrp 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 SerGlyValCysGlyAsnAsnAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 GluHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTGTTTTTTGCTGCT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lidary, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Roseherger, Cindy A.
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCE ADDRESS:
ADDRESSED: Charles E. Cohen, Monsanto Company, BB4F
STREE: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-FOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-006-252A-19 (1-414) x US-08-627-706-15 (1-79)
              ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 34,565
TELECOMMUNICATION INFORMATION:
TELEPROX: (314,1537-6047
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
Gaps:
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APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UTN-1998
FILING PATE: 800
ATTORNEY/AGENT INFORMATION:
NAME: COhen, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        396.50
96.25$
88.75$
52.73$
                                                                                                                                                                                                                  LENGTH: 79 amino acids
                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-627-706-15
                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG 135
                                                                                                                                      136 rcaggagrergrgaaacaaraacgeargcaagaarcagrgcarraaccrrgagaaagca 195
                                                                                                                                                                                               196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTAGTTTTCCTTGT 255
                                         21 PheGlualaProThrMetValAspAla---ArgleuCysGluArgProSerGlyThrTrp 39
                          40 SerGlyValCysGlyAsnAsnAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: BIM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
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Conservative:
Mismatches:
Indels:
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Facent No. 5538525
GENERAL INFORMATION:
APPLICANT: BROEKABET, WILLEM F.
APPLICANT: CANWIG, BRUNO P.A.
APPLICANT: CANWIG, REEK, W. APPLICANT: TEREAS, FRANE W.
APPLICANT: TEREAS, FRANE W.
APPLICANT: TEREAS, FRANE W.
APPLICANT: TEREAS, FRANE R.G.
APPLICANT: VANDELEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN DAMBY & CUSHWAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STRAT: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
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309.00
100.00%
100.00%
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MOLECULE TYPE: peptide
US-08-377-687-19
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Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 TCAGGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
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71
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION NUMBER: 34,565
REPERBENE JOCKET NUMBER: 38-21 (10700) A
TELECOMUNICATION INFORMATION:
TELEPACNE: (314) 537-624
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   1.58e-39
396.50
96.25%
88.75%
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396.50
96.25%
88.75%
52.73%
                                                                                                 LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                            ) TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-09-103-489-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Alyssum Sp.
US-09-829-381D-15
                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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US-09-829-381D-15
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103 CAGAAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCA 162
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                                                                                                               1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
                                                                                                                                                                                                                                                      21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NS-08-627-706-18

Sequence 18, Application US/08627706

Fatent No. 577369

Fatent No. 577369

FAPLICANT: Liang, Jihong

APPLICANT: Bah, Dilip M.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19

CORRESPONDENCES: 19

CORRESPONDENCES: Charles E. Cohen, Monsanto Company, BB4F

STREET: 700 Chesterfield Village Parkway No. 5773696th

CITY: St. Louis

STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentl Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/627,706
FILING DATE:
CLASSIFICATION NUMBER: 34,565
ATTONNEY/AGENT INFORMATION:
NAME: COHEN, Charles E.
REGISTRATION NUMBER: 34,565
REGISTRATION NUMBER: 34,565
REGISTRATION NUMBER: 34,565
REGISTRATION NUMBER: 31,565
REGISTRATION POR SEQ 1D NO: 18:
SEQUENCE CHARACTERISTICS:
THATTHER SEQUENCE CHARACTERISTICS
THATTHER SEQUENCE CHARACTERISTICS
THATTHER SEQUENCE CHARACTERISTICS
THATTHER SEQUENCE CHARACTERISTICS
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Matches:
Conservative:
Mismatches:
US-10-006-252A-19 (1-414) x US-08-377-687-19 (1-51)
                                                                                                                                                                                                                                                                                                                                                                     223 CCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-006-252A-19 (1-414) x US-08-627-706-18 (1-51)
                                                                                                                                                                                                                                                                                                                                                                                                         41 ProAlaHisLysCysIleCysTyrPheProCys 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
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309.00
100.00$
110.00$
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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DB:
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Db 21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe 40
Cy 223 CCAGCTCACAAGTGTATCTGCTACTTGCTTGT 255
Cy 223 CCAGCTCACAAGTGTATCTGCTACTTGCTTGT 255
Db 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Search completed: May 11, 2004, 17:06:19
Job time: 27 secs
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Sequence 49, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 12, Appl Sequence 14, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 19, Appl Sequence 19, Appl Sequence 34, Appl Sequence 34, Appl Sequence 31, Appl Sequence 33, Appl Sequence 31, Appl Sequence 56, Appl Sequence 56, Appl Sequence 57, Appl
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Sequence
Sequence
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                                                                                                                                                                                                                                           US-09-759-584-19
US-09-732-561-19
US-10-681-972-18
US-10-388-361A-34
US-10-056-252-22
US-10-072-809A-33
US-10-072-809A-35
US-10-072-809A-35
US-10-072-809A-35
US-10-072-809A-35
US-10-06-252A-59
US-10-06-252A-65
US-10-06-252A-79
US-10-06-252A-79
US-10-06-252A-79
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US-10-06-252A-79
9 US-09-759-584-49

9 US-09-829-381A-20

12 US-10-681-972-20

9 US-09-759-584-59

12 US-10-732-561-14

12 US-10-63-396-13

9 US-09-732-561-14

12 US-10-63-396-13

13 US-10-63-396-13

14 US-10-63-381A-18

15 US-09-829-381A-18

16 US-10-88-361-37

17 US-10-681-972-18

18 US-10-681-972-18

19 US-09-759-584-19

10 US-10-681-972-18

11 US-10-681-972-18

12 US-10-78-809A-33

13 US-10-006-252A-57

13 US-10-06-252A-57

13 US-10-06-252A-57

13 US-10-06-252A-61

13 US-10-06-252A-61

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17 US-10-06-252A-61

18 US-10-06-252A-61

19 US-10-06-252A-28

11 US-10-06-252A-28

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18 US-10-06-252A-28

19 US-10-06-252A-28

10 US-10-06-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMIE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SECURNOES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET LOOPEN SOR AVENUE, N.W. STREET 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 49, Application US/09759584
Patent No. US20010014732A1
GENERAL INFORMATION:
  20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-09-759-584-49
    Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-DEPC=2026/4pp_query.fasta_1.583
-DE=Published_Applications_AA -QFWT=fasta_1 -SUFFXX=rapb -MINMATCH=0.1
-LOCPEXT=0 -LOCPEXT=0 -UNITS=bits -START=1 -BND=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR MXS=cot -THR MXX=10
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptc -NORM=ext -HBARSIZE=500 -MINLEN=0
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptc -NORM=ext -HBARSIZE=500 -MINLEN=0
-NCPU-6 -ICPU-3 -NO MMAP -LARGEQUERY NGS GCGN 1 113 @runat 11052004 141659 22867
-NCPU-6 -ICPU-3 -NO MMAP -LARGEQUERY NGS GCGN 20 -THREADS=1 -XGAPDFHLOCK=100
-LONGLOG -DEV TIREOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5
-FGAROP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                          May 11, 2004, 17:02:19 ; Search time 41.5 Seconds (without alignments) 5537.958 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                  - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1140673 seqs, 277566755 residues
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Minimum DB seq length: 0 Maximum DB seq length: 200000000

0.5

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

Searched:

**BLOSUM62** 

US-10-006-252A-19 752

Perfect score: Scoring table:

Title:

Sequence:

nucleic

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Run on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Query Score Match Length DB

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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGAAGTGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Younie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       880000
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
                                                                                                                                                                                                                                      99042/SEE.36525/US/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-006-252A-19 (1-414) x US-09-759-584-49 (1-80)
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Matches:
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Sequence 20, Application US/09829381A

Patent No. US20020144306A1

GENERAL INFORMATION:
                                                                                                                            ATTORNEY, AGENT INFORMATION:
NAME: KOKULIS, PAIL N.
REGISTRATION NUMBER: 16,773
REFERENCE, DOCKET NUMBER: 99042
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-861-300
TELEFAX: 202-861-300
TELEFAX: 202-862-0944
; INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION.NUMBER: 08/377,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        442.00
100.00%
100.00%
58.78%
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STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-759-584-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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DB:
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Sequence 20, Application US/10681972

Publication No. US20040064850A1

Publication No. US20040064850A1

Publication No. US20040064850A1

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Yonnie S.

TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION NUMBER: US/10/681,972

CURRENT FILING DATE: 2001-04-09

PRIOR FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 TICGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION SATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:

NAME: COHO, CHAPIES IS

REGISTRATION NUMBER: 34,565

REGISTRATION NUMBER: 34,565
TELERBONE: (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-829-381A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score: 434.00
Percent Similarity: 98.75%
Best Local Similarity: 98.75%
Query Match: 57.71%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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US-10-681-972-20
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LENGTH: 80
TYPE: PRT
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protein

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MOLECULE TYPE:
                     US-09-759-584-59
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DB:
                                                                                 . No. :
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                                                                                                                                                                                                                                                                                                                                                                                                             41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
                                                                                                                                                                                                                                                                21 PheGluhlagluThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA ZIP: 20005 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATCHIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: US/09/759,584
                                                                             0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE:
TILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: XOKULIS, PAUL N.
FREGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFANE: 202-62-9044
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                    US-10-006-252A-19 (1-414) x US-10-681-972-20 (1-80)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 59, Application US/09759584

Patent No. US20010014732A1

GENERAL INFORMATION:
APPLICANT: BROBKAERT, WILLEM F.
APPLICANT: CAMMUS, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: APPLICANT: TERRS, SARAH B.
APPLICANT: TERRS, FRANKX R.G.
APPLICANT: VANDELEYDEN, JOZEF
TILLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                      Gaps:
                                                                       6.28e-41
434.00
98.75$
98.75$
; ORGANISM: Raphanus sativus
US-10-681-972-20
                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                        Alignment Scores:
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US-09-759-584-59
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                                                                                                                              1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
                                                                                                                                                                             21 PheGlualaProThrMetValGlualaGlnLysLeuCysGlnArgProSerGlyThrTrp
                                                                                                                                                                                                           136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
                                                                                                                                                                                                                           41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla
                                                                                                                                                             76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCCAAGTGGGACATGG
                                                                                                                  16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTGCTGCT
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            Length:
Matches:
Conservative:
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Indels:
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                           US-10-006-252A-19 (1-414) x US-09-759-584-59 (1-80)
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                                                                       Gaps:
          8.18e-41
433.00
98.75%
97.50%
57.58%
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417.00
95.00%
92.50%
55.45%
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; ORGANISM: Raphanus sativus
US-10-636-396-21
                                Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Query Match:
DB:
Alignment Scores:
Pred. No.:
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136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
21 PheGlugluProThrMetValGluAlaGlnLySLeuCysGlnArgProSerGlyThrTrp 40
                                                                                 41 SerGlyValCysGlyAsnAsnAsnAsnAsnCysLysAsnGlnCysIleArgLeuGluLysAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
                                                                                                                                                                   Sequence 16, Application US/09732561
Sequence 16, Application US/09732561
Septement No. US20020035738A1
SENELL INFORMATION:
APPLICANT: Thomma, Bart
APPLICANT: Terras, Franky
APPLICANT: Pernainckx, Iris
APPLICANT: Manners, John
APPLICANT: Manners, John
APPLICANT: Razan, Kemal
APPLICANT: Razan, Kemal
APPLICANT: Broekaert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: ZENECP.
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Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION VUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
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APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
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Best Local Similarity:
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US-10-006-252A-19 (1-414) x US-09-732-561-16 (1-80)

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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAGTGTATCTGCTACTTTCTTGT 255
16 AIGGCIAAGITIGCGICCAICAICGCACTICITITIGCIGCICTIGITCITITITGCIGCT 75
                                                                 21 PheAspAlaProAlaMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80
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ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/09/732,561
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
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US-09-732-561-22
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Sequence 22, Application US/09732561

GENERAL INFORMATION:
APPLICANT: Thomma, Bart
APPLICANT: Tromma, Bart
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Manners, John
APPLICANT: Macan, Kemal
APPLICANT: Reach, Kemal
APPLICANT: STREET: 1800 Concerned application Method
CORRESPONDENCE ADDRESS:
STREET: 1800 Concerned application Concerned Concern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
Conservative:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REGISTRATION NUMBER: 33,712
REFERENCE/LOCKET NUMBER: PPD 50165/UST
TELECOMONICATION INFORMATION:
TELECOMONICATION 100: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids

"THE CHARACTERISTICS:
LENGTH: 90 amino acids
"THE CHARACTERISTICS:
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
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STATE: DE
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Query Match: 53.59% Indels: 0 DB: 9 Gaps: 0	Align	Alignment Scores: Pred. No.:
US-10-006-252A-19 (1-414) x US-09-732-561-22 (1-80)	Score	e: ent Similarity
16 AIGGCTAAGTITGCGTCCAICATGCGCACTICTITTGCTGCTCTTGTTTTTGCTGCT 75	Best Query DB:	Best Local Similar Query Match: DB:
	us-10	US-10-006-252A-19 Qy 16 ATGG
	g &	1       1 Met.A. 76 TTCG
196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCAAGTGTATCTGCTACTTTCTTT	qa	21 Leug
	ð í	
RESULT 8 US-09-722-561-14 Sequence 14, Application US/09732561 ; Patent No. US20020035738A1	음 & 음 ·	41 SerGl 196 CGACF 
ENERAL INFORMATION: APPLICANT: Thomas Bart APPLICANT: Terrae Bart	RESULT	6 E
Penninch Manners,	US-10 ; Seq	US-10-636-396-23 ; Sequence 23, Appl : Publication No. II
APPLICANT: Kazan, Kemal APPLICANT: Broekert, Willem	GEN	GENERAL INFORMATI APPLICANT: Bidne
ILLE OF INVENTION: Plant Protection Method NUMBER SEQUENCE: 24 CORRESPONDENCE: 24	AP ;	PLICANT: Cras
ADDRESSEE: ZENECA AG Products STREET: 1800 Concord Pike	, AP ; AP	APPLICANT: Hu, APPLICANT: Lu, TITLE OF INVENTI
STATE: DESCONTRY: USA		TLE OF INVENTI LE REFERENCE: PPENT APPLICAT
ZIP: 19850 COMPUTER RESIDELE FORM: MEDITIN WYDE. PLACES	388	RRENT FILING DIOR APPLICATION
CHARTER IN TORON GIBK COMPANYTOR IN TORON GOVERNMENT OF COMPANY OF	 R. E. E.	IOR FILING DAT
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:	 P. P. P. R. P. R. P. R. P. P. R. P.	PRIOR FILING DAT PRIOR APPLICATIO PRIOR FILING
APPLICATION NUMBER: US/09/732,561 FILING DATACHER: GRANDELER:	SOS :	NUMBER OF SEQ ID SOFTWARE: FastSE
PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/202,638	SEO	SEQ ID NO 23 LENGTH: 80 TVDE: DPT
FILING DATE: PRIOR APPLICATION DATA: APPLICATION NIMPER: Detrices	; ; ; ; ; ; ;	, ORGANISM: Arabi US-10-636-396-23
FILING DATE: 20-JUN-1997 ATTORNEY/AGENT INFORMATION:	Alignment	ment Scores:
NAME: Hohenschutz, Liza D. REGISTRATION NUMBER: 33,712	Pred. Score: Percen	Pred. No.: Score: Percent Similarity:
KEFERENCE/DOCKET NUMBER: PPD 50165/UST TELECOMMUNICATION INFORMATION: TELEPHONE: (302) 886-11999 INFORMATION FOR SEC ID NO: 14.	Best   Query DB:	Best Local Similari Query Match: DB:
02	US-10	US-10-006-252A-19 (
TYPE: amino acid TYPE: amino acid monor.com	ò	16 ATGGC
JOCOLOGI: linear MOLECULE TYPE: protein	QQ	1 MetAla
CALGLIAND SOURCE: STAIN: PDF1.1	Š	76 TTCGA
-/32-561-14	qq	21 Leugli

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PARGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGCCCAAGTGGGAACATGG 135
                                                                                                                                                                               GGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
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asta, Oswald R.
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Guihua
TION: Sunflower Anti-Pathogenic Proteins and
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Matches:
Conservative:
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G DATE: 2003-08-07
TION NUMBER: US/09/589,733C
DATE: 2000-06-08
TION NUMBER: 60/140,646
DATE: 1999-06-23
TION NUMBER: 60/162,904
DATE: 1999-11-01
ID NOS: 41
TSEQ for Windows Version 3.0
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US20040073971A1
FION:
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136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                            196 GACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
                                                                                                   61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS;
ADDRESSEE: TOO. Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                  nu, increase. Cindy A. Rosenberger, Cindy A. Rosenberger, Cindy A. TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IEBS FOC COMPATIBLE
COMPUTER: IEBS FOC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <UNKOWN>
PRIOR APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORIEY/AGENT INFORMATION:
APPLICATION NUMBER: 09/103,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCS/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-006-252A-19 (1-414) x US-09-829-381A-15 (1-79)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
WOLECTLE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                    Sequence 15, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 79 amino acids
                                                                                                                                                                                                                                                                 APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 63198
COMPUTER READABLE FORM:
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96.25%
88.75%
52.73%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                               US-09-829-381A-15
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DB:
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Sequence 15, Application US/10681972
| Publication No. US20040064850A1
| Publication No. US20040064850A1
| GENERAL INPORMATION
| APPLICANT: Liang, Jihong
| APPLICANT: Shah, Dilip M. APPLICANT: Shah, Dilip M. APPLICANT: Wu, Yonnie S. TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
| FILE REFERENCE: 38-21 (10700) C | CURRENT FILING DATE: 2003-10-09 |
| FILE REFERENCE: 38-21 (10700) C | CURRENT FILING DATE: 2001-04-09 |
| FRIOR APPLICATION NUMBER: US/09/829,381D |
| PRIOR FILING DATE: 1998-06-24 |
| NUMBER OF SEQ ID NOS: 20 |
| SEQ ID NOS: 20 |
| SEQ ID NO 15 |
| LENGTH: 79 |
                                                                                                     196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAGTGTATCTGCTACTTTCTTGT 255
136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                         40 SerGlyValCysGlyAsnAsnAsnAsnAsnAshaCysArgAsnGlnCysArgAsnLeuGluArgAla 59
                                                                                                                                 60 GluHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 SerglyValCysGlyAsnAsnAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 PheGluAlaProThrMetValAspAla---ArgLeuCysGluArgProSerGlyThrTrp 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GluHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 71 72 71 73
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-006-252A-19 (1-414) x US-10-681-972-15 (1-79)
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APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 19, Application US/09759584; Patent No. US20010014732A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BROEKAERT, WILLEM F. APPLICANT: CAMMUE, BRUNO P.A. APPLICANT: OSBORN, RUPERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396.50
96.25$
88.75$
52.73$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Alyssum Sp.
US-10-681-972-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                        RESULT 11
US-10-681-972-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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US-09-759-584-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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1800 Concord Pike

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STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 IGCAAGAATCAGIGCATTAACCTIGAGAAAGCACGACAIGGATCITGCAACTAIGICTIC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAla
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                                                                                                                                                                                                  ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION UMBER: US/09/759,584
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Terras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Kaan, Kemal
APPLICANT: Kaan, Kemal
APPLICANT: Kemal
APPLICANT: Brockaert, Willem
IITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECR AG Products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 CCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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                  CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: XCMULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SE
TELECHONNICATION INFORMATION:
TELECHONE: 202-861-3000
TELEFRAX: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/09732561
Patent No. US20020035738A1
GENERAL INFORMATION:
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100.00%
100.00%
41.09%
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
NUMBER OF SEQUENCES:
                                                                                                                WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                CITY: WASHII
STATE: D.C.
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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US-09-732-561-19
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103 CAGAAGTIGIGCGAAAGGCCCAAGTGGACAIGGTCAGGAGTCTGTGGAAACAATAACGCA 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0000
                                                   ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                              FILING DATE:

(LASSIFICATION NUMBER: US/US/134, 561

CLASSIFICATION E

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/202,638

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB97/01672

FILING DATE: 20-UN-1997

ATOMNE: Hohenschutz, Liza D.

REGISTRATION NUMBER: 9DD 50165/US'

REGISTRATION NUMBER: 33,712

REGERROCHOCKET NUMBER: PPD 50165/US'

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 886-1699

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 51 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/09829381A
Patent No. US2020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309.00
100.00%
100.00%
41.09%
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IMMEDIATE SOURCE:
CLONE: Rs-AFP1
Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                        USA
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US-09-829-381A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-732-561-19
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Sequence 18, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Contro;
TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE OF INVENTION: Plant Pathogenic Fungi
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION WHORER: US/09/829,381D
PRIOR APPLICATION NUMBER: 09/103,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 CAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 TGCAAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe 40
700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                           CURRENT APPLICATION DATA

APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-54Dr-2001
CLASSIFICATION NUMBER: US/09/829,381A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: COHEN, Charle E.
RESTSTRATION NUMBER: 34,565
REPERENCE/DOCKEY NUMBER: 38-21 (10700) A
TELECOMMUNICATION INFORMATION:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 ProAlaHisLysCysIleCysTyrPheProCys 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-829-381A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.28e-26
309.00
100.00%
100.00%
                                                                              ZIP: 63198
COMPUTER READABLE FORM:
           CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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Best Local Similarity:
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103 CAGAAGTTGTGCGAAAGGCCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCA 162
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Job time: 42.5 secs
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 51
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                                                                      TYPE: PRT; CRGANISM: Raphanus sativus
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 May 11, 2004, 16:59:19 ; Search time 18.5 Seconds (without alignments) 4305.221 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Tillingal protein I precursor - radish
C;Species: Raphanus sativus (radish)
C;Species: Raphanus sativus
C;Accession: Tilling
R;Persasion: Tilling
A;Plant Cell 7, 568-573, 1955
A;Plate: Small cysteine-rich antifungal proteins from radish: their role in host def.
A;Reference number: Z16976
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A;Rocession: Tilling
A;Rolecule type: mRNA
A;Reference: Entain ronde rode kleine witpunt; tissue type seed
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A;Reference: Entain ronde rode kleine witpunt; tissue type seed
A;Rolecule type: MRNA
A;Reference: Entain ronde rode kleine witpunt; tissue type seed
A;Rolecule type: Daylor: Schoofs, H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.B.; Vanderley, J. Biol. Chem. 267, 1530-15309, 1992
A;Residues: Gf. usalysis of two novel classes of plant antifungal proteins from radish (Rapi A;Rocession: A4284
A;Recession: A4284
A;Recession: A4284
A;Residues: 30-73 < TE2>
A;Residues: Seed
A;Rote: sequence extracted from NCBI backbone (NCBIP:109570)
A;Gene: ARPI
C;Punction:
A;Gene: ARPI
C;Punction: A;Gene: ARPI
C;Function: A;Gene: ARPI
C;Reme: ARPI

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Length

Query Match

Result Š. F;1-29/Domain: signal sequence #status predicted <SIG> F;30-80/Product: antifungal protein 1 #status predicted <MAT>

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Length:

1.8e-39

Alignment Scores: Pred. No.:

antifungal protein hypothetical prote antifungal protein antifungal protein defensin AMPI - Da

G86328 S28989 S28995 S66221

antifungal protein probable antifunga probable antifunga antifungal protein antifungal protein

Description

protein T4012.7 [i antifungal protein antifungal protein probable antifunga

T10183 T02621 T02622 F96787 T07917 T10243 F96591

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3399 3999 3999 393.55 1075 1156 156

	Oy         196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTGCAAGTGTATCTGCTACTTCCTTGT         255           Db         61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys         80	RESULT 3 T10183 antifungal protein 4 precursor - radish C;Species: Raphanus sativus (radish) C;Species: Raphanus sativus radish C;Bers. 16.Thilloo #seminara radish	n, R.W.; Broe	A; Accession: T10183 A; Accession: T10183 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRN; translated from A; Molecule type: mRN; A; Molecule type: mRN; A; Molecule type: mRN; A; Molecule type: TPR; A;	A;Cross-references: EMBL:X97318 A;Experimental source: cultivar Ronde Rode Kleine Witpunt C;Genetics: A;Gene: AFP4 C;Superfamily: gamma-thionin C;Keywords: antifungal F;1-29*Domain: signal sequence #status predicted <sig></sig>	880 72 72 6	-10-006-252A-19 (1-414) x T10183 (1-80) 16 ATGGCTAAAGTTTGCTCCATCATCGCACTTCTTTTGCTGCTTGTTCTTTTTGCTGCT	Db 1 MetAlaLysPheValSerIleIleThrLeuLeuPheValAlaLeuValLeuFheAlaAla 20 Oy 76 TTCGAAGACACAACAATGGTGGAAGCACAGAAGGCCAAGTGGCGAAGAGCCAAGTGG 135	TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 19 	Qy 196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255	16-Feb-2001	K;Kounsley, S.L.; Adul, S.; Lun, A.; McConum, N.A.; Closby, M.L.; Brandon, N.C.; submitted to the EMBL Data Library, August 1987. A;Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence. A;Reference number: Z14681 A;Accession: T02621 A;Molecule type: DNA A;Residues: 1-80 <rou></rou>
ore: 442.00 rcent Similarity: 100.00\$ st Local Similarity: 100.00\$ ery Match: 58.78\$	US-10-006-252A-19 (1-414) x T10176 (1-80) QY	76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCCAAGTGGGACATGG	Oy 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195	Qy 196 CGACATGGAPCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255	T10823 antifungal protein 2 precursor - radish c;Species: Raphanus sativus (radish) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000 C;Accession: T10823; B42842 C;Accession: F.R.; Begermont, K.; Kovaleva, V.; Raikhel, N.V.; Osborn, R.W.; Kester, A.; Re	sh: their role	R,Terras, F.R.; Schoofs, H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.B.; Vanderleyden, J. Biol. Chem. 267, 15301-15309, 1992 A,Title: Analysis of two novel classes of plant antifungal proteins from radish (Raphanu A,Reference number: A42842; MUID:92348373; PMID:1639777 A;Accession: B42842	A;Status: preliminary A;Nolecule type: protein A;Residues: 30-65 <te2> A;Experimental source: seed A;Note: sequence extracted from NCBI backbone (NCBIP:109572)</te2>	C:Geneilos: A;Gene: AFP2 C;Function: has antifungal activity C;Superfamily: gamma-thionin	F;1-43/Domain: signal sequence #status predicted <sig> F;44-80/Product: antifungal protein 2 #status predicted <mat></mat></sig>	Pred. No.: 9.13e-37 Length: 80 Score: 417.00 Matches: 74 Percent Similarity: 95.00% Conservative: 2 Best Local Similarity: 92.50% Mismatches: 4 Query Match: 2 DB: 2	US-10-006-252A-19 (1-414) x T10823 (1-80)  QY

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in, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, & brary, August 1998
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AACTATGTCTTCCCGGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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                                                                                                                           revision 16-Jul-1999 #text_change 20-Jun-2000
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na (mouse-ear cress)
_revision 24-Mar-1999 #text_change 16-Feb-2001
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protein T4012.7 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Parabidopsis thaliana (mouse-ear cress)
C;Accession: F96787
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Venter, J.C.; Davis, M.; Sun, H.; Tallc A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Retence number: P86787
A;Scatus: preliminary
A;Molecule type: DNA
A;Restus: preliminary
A;Molecule type: DNA
A;Restus: Pareliminary
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C;Genetics:
A;Gene: T4012.7
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                 A;Gene: At2g26010; T19L18.18
A;Map position: 2
A;Introns: 22/1
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A,Cross-references: EMBL:AC004747; NID:g3413696; PID:g3413721
A,Experimental source: cultivar Columbia
R,Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Gronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Nature 402, 761-768, 1999
A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A,Reference number: A84420; MUD:20083487; PMID:10617197
A,Rocession: B84655
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-80 <270>
A,Cross-references: GB.AE002093; NID:g3413721; PIDN:AAC31244.1; GSPDB:GN00139
A,Genetics:
C,Genetics:
A,Map position: 2
A,Introns: 22/1
C;Superfamily: gamma-thionin
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Cincession: F96591

Theologis, A.; Ecker, U.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudhes, B.; Hudzar, L.
Abature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A; Rzonew, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Snim, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Reference and analysis of chromosome 1 of the plant Arabidopsis.

A; Accession: F96591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable antifungal protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
                                          F;30-79/Product: antifungal protein 3 #status predicted <MAT>
            F;1-29/Domain: signal sequence #status predicted <SIG>
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Mismatches:
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C;Superfamily: gamma-thionin
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Best Local Similarity:
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A; Molecule type: DNA
A; Residues: 1-80 <STO>
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antifungal protein 3 precursor - radish
c;Species: Raphanus sativus (radish)
c;Date: 16-Uul-1999 #sequence_revision 16-Uul-1999 #text_change 20-Jun-2000
c;Accession: T10243
R;Terras, F.R.G; Goderis, I.J.; Penninckx, I.J.; Osborn, R.W.; Broekaert, W.F.
submitted to the EMBL Data Library, April 1996
A;Reference number: 216994
A;Accession: T10243
A;Status: prellminary; translated from GB/EMBL/DDBJ
A;Residues: 1-79 <TER>
A;Residues: 1-79 <TER>
A;Residues: 1-79 <TER>
A;Creas: references: EMBL: S97319
A;Creas: references: EMBL: S97319
C;Genetics:
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21 LeuGlualaProMetValValGlualaGlnLysLeuCysGluArgProSerGlyThrTrp 40
                                                                                                                                                    41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
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                                                                                                                                                                                                                                                                                                                                                                                       antifugal protein - rape (Species: Brassica napus (rape) (Species: Brassica napus (rape) (Species: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jun-2000 (SAccession: T07917 Risohn, U.; Lee, C.M.; Lee, M.H.; Kim, J.H. Risohn, U.; Lee, C.M.; Lee, M.H.; Kim, J.H. A.Reference number: 216214 A.Reference number: 216214 A.Reference number: 216214 A.Reference number: 2017 A.Residues: preliminary; translated from GB/EMBL/DDBJ A.Residues: 1-79 <SOH>
C.Superfamilly: gamma-thionin
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Matches:
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2.49e-34 394.50 93.75% 91.25% 52.46%

Percent Similarity: Best Local Similarity:

Query Match: DB:

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Alignment Scores:

A,Gene: AFP3 C,Superfamily: gamma-thionin C,Keywords: antifungal

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antifungal protein 1 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
C;Accession: 328928; P.B.G; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Camm FEBS Lett. 316, 233-240, 1993
A;Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicac A;Accession: $28995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CjAccession: S28989

RjTerras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Can FEBS Lett. 316, 233-240, 1993
A;Title: A new family of basic cysteine-rich plant antifungal proteins from Brassica A;Reference number: S28989; MUID:93138130; PMID:8422949
A;Recession: S28989; MUID:93138130; PMID:8422949
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-27 <TER>
C;Superfamily: gamma-thionin
                                                                                                                                                                                                                                                                                                                                              166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACGATGGATCTTGCAACTATGTCTTCCCA 225
                                                                                                                                                                                                                                                 106 AAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 165
                                                                                                                                                                                                                                                                                                                                                                        antifungal protein 1 - turnip (fragment)
C;Species: Brassica rapa (turnip)
C;Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
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C;Species; Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: G36328
R;Theologis, A.; Ecker, J. R; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, X.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 1816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowarz, J.S. Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwarzz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: A86141; WUID:21016719; PMID:11130712
A;Reseronce number: A86141; WUID:21016719; PMID:11130712
A;Residues; 1.56 cSTC)
A;Residues; 1.56 cSTC)
                                                                                                                                                                                                                                                                                                                   antifungal protein 1 - rape (fragment)
C;Species: Brassica napus (rape)
C;Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
C;Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
C;Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
R;Accession: S.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, FEBS Lett. 316, 233-240, 1993
A;Afitle: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae
A;Reference number: S28989; MUID:93138130; PMID:8422949
136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                            196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAG---TGTATCTGCTACTTTCCT 252
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                                             40 SerGiyArgCysValAsnAspTyrGlnCysArgAspHisCysileAsnAsnAspArgGly 59
                                                                                                                            1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAla 20
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A, Residues: 1-30 <TER>
A, Accession: S28992
A, Molecule type: protein
A, Residues: 1-23 <TE2>
C, Superfamily: gamma-thionin
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Best Local Similarity:
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A,Map position: 1
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N;Alternate names: seed antifungal protein

N;Alternate names: seed antifungal protein

C;Decies: Dahlia merckii

C;Decies: Dahlia merckii

C;Decies: Dahlia merckii

C;Species: Dahlia merckii

R;Cspecies: Dahlia merckii

R;Cspecies: N; Gscallia merckii

R;Cspecies: N; Gscallia merckii

R;Cspecies: Seedules: Seedules: Seedules: Seedules: Seedules: Seedules: Seedules: Seedules: Seedules: Teacher merckii

R;Residules: 1-50 coss

C;Resywords: antifungal
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C;Species: Sinapis alba (white mustard)
C;Species: Sinapis alba (white mustard)
C;Date: 25-F891994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
C;Accession: S289193
R;Terras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, FEBS Lett. 316, 233-240, 1993
A;Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae A;Reference number: S28989; MUID:93138130; PMID:8422949
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-25 <TER>
C;Superfamily: gamma-thionin
                                                                                                                                                                              106 AAGTIGIGGAAAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 165
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1 GluLeuCysGluLysAlaSerLysThrTrpSerGlyAsnCysGlyAsnThrGlyHisCys 20
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                   Conservative:
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      Mismatches: 0

      Query Match: 2
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      Indels: 0
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      DB: 2
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      CS-10-006-252A-19 (1-414) x $28993 (1-25)

      QY
      103 CAGAAGTTGTGCGAAAGGCCAAGTGGCACATGGTCAGGAGTCTGTGGAAACAATAACGCA 162

      DD
      1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAsnAsnAla 20

      QY
      163 TGCAAGAATCAGTGC 177

      CYSLysAsnGlnCys 25
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Search completed: May 11, 2004, 17:05:18 Job time : 19.5 secs

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

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P14585 caenorhabdi
P35556 homo sapien
P18168 drosophila
P78990 kluyveromyc
Q90y54 brachydanio
                                           vigna ungui
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pisum sativ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica napus (Rape), and
Raphanus sativus (Radish).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae, Brassica.
NCBI_TaxID=3708, 3726;
                                                                                                                                                                                                                                                                                  rattus
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SPECIESER. satisfurus; IISSUE-Seed;
MEDLINE-92348373; PubMed=1639777;
Terras F.R.G., Schoofs H.M.E., de Bolle M.F.C., van Leuven F.,
Rees S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
"Analysis of two novel classes of plant antifungal proteins from radish (Raphanus sativus L.) seeds.",
Q43413 G
Q9zul8 B
P1846 F
Q01784 E
Q01783 E
Q65717 G
Q95718 G
Q95718 G
Q95718 G
P81929 E
P10914 E
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P81930
Q8cg18
Q8cg19
P20346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                NTCI_RAT
PSD2_PEA
LTBS_MOUSE
LTBL_MOUSE
P322_SOLTU
LI12_CAEEL
FBN2_HUMAN
                                                                                                                                                                                                              PSD1 PEA
THG2 ARATH
DL DROME
                                                                                                                                                                                                                                                              DL DROME
LEM3 RAT
DEF2 SPIOL
THGF HELAN
ASF2 HELAN
  DEFI CAPAN
10KD ARATH
10KD DR39 PEA
D230 PEA
AD02 MOUSE
THG3 ARATH
THG1 ARATH
THG1 ARATH
AX2 EETVU
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MEDLINE=93138130; PubMed=8422949;
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  SEQUENCE FROM N.A.
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096123 arabidopsis
080994 arabidopsis
080995 arabidopsis
080995 arabidopsis
030313 brassica na
024332 raphanus sa
P30231 sinapis alb
010969 sinapis alb
P3022 brassica ra
P22357 brassica ra
P2235 helianthus
P3022 brassica na
024115 nicotiana p
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P30230 raphanus sa
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3079.578 Million cell updates/sec
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

    protein search, using frame_plus_n2p model

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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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AFP1
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Maximum DB seq length: 2000000000
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Match Length DB
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BRARA

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Result

Database :

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eurosids II; Brassicales; Brassicaceae; Raphanus.
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                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
J. Biol. Chem. 267:15301-15309(1992).
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYSTEINE-RICH ANTIFUNGAL PROTEIN 1.
PYRROLIDONE CARBOXYLIC ACID.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
05B90FAAC8DAC2B CRC64;
                                                              -!- SUBUNIT: Forms oligomers in its native state.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 2 precursor (AFP2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PP00304; Gamma-thionin; 1.
SMART. 20005594; G Purothionin; 1.
PROSITE, PS00940; GAMMA_THIONIN; 1.
PROSITE PS00940; GAMMA_THIONIN; 1.
Pyrrolidone carboxylic acid. Signal; Multigene family; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P30231; 1AXJ.
InterPro, IPR008176; Gamma-thionin.
InterPro; IPR003614; Knotl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                        EMBL; U18557; AAA69541.1; -.
PIR; T10176; T10176.
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30
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76
8734 MW;
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Best Local Similarity:
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Pred. No.:
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ID AFP2 RA
DT 01-APR.
DT 01-APR.
DT 28-FEB.
DE Cysteil
GN AFP2.
OS Raphan
OC Sukary.
OC Sukary.
SOUND THE FEET FEET AND THE SOUND TO SOUND THE SOUND TO SOUND THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 AIGGCIAAGITIGCGICCAICAICGACTICITITIGCIGCICTICITITIGCIGCI
                                                                                                            Terras F.R.G., Eggermont K., Kovaleva V., Raikhel N.V., Osborn R.W., Kester A., Rees S.B., Torrekens S., van Leuven F., Vanderleyden J., Cammue B.P.A., Broekaert W.F.; "Small cysteine-rich antifungal proteins from radish: their role in host defense."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                 TISSUE=Seed;
MEDINE=92348373; PubMed=1639777;
MEDINE=92348373; PubMed=1639777;
Terras F.R.G., Schoofs H.M.E., de Bolle M.F.C., van Leuven F.,
Rees S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
"Analysis of two novel classes of plant antifungal proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYSTEINE-RICH ANTIFUNGAL PROTEIN 2. PYRROLIDONE CARBOXYLIC ACID.
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746110D9A8CE6370 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
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RNOSTER; PS00540; GAMMA THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family;
Pyrrolidone carboxylic acid.
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                                           SEQUENCE FROM N.A.
STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
MEDLINE=95299350; PubMed=7780308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (Raphanus sativus L.) seeds."
.. Chem. 267:15301-15309(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U18556; AAA69540.1; -.
PIR; T10823; T10823.
HSSP; P30231; 1AVJ.
INCEPPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
Pfam; PF00304; Gamma-thionin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD002594; G_Purothionin; 1.
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417.00
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55.45%
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NCBI_TaxID=3726;
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AFP4\_RAPSA 024331;

AFP4 RAPSA

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                                                                                                                                    TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                  196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
          1 MetAlaLysPheValSerIleIleThrLeuLeuPheValAlaLeuValLeuPheAlaAla 20
                                                                                                                                                                                                                                            61 ArgHisGlySerCysAsnTyrIlePheProTyrHisArgCysIleCysTyrPheProCys 80
                                                                                21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgSerSerGlyThrTrp
                                                                                                                                                                  41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla
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                                                    TTCGAAGCACCAACAATGGTGGAAGCACAGAGTTGTGCGAAAAGGCCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structural analysis of Arabidopsis thaliana chromosome 5. IX. Sequence features of the regions of 1,011,550 bp covered by seventeen P1 and TAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                core eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vanoosthuyse V., Miege C., Dumas C., Cock J.M.;
Submitted (JUN-2000) to Swiss-Prot.
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CV. Columbia;
MEDLINE=99397451; PubMed=10470850;
KARDEKO T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
Miyajima N., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                         AFP4_ARATH STANDARD; PRT; 80 AA.
09F123. P82786, 4
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable cysteine-rich antifungal protein LCR77 precursor (AFP).
LCR77 OR AT5G44420 OR MFC16.8
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cations (By similarity).
--- SUBCELLULAR LOCATION: Secreted (By similarity).
--- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spermatophyta; Magnoliophyta; eudicotyledons; core everosids II; Brassicales; Brassicaceae; Arabidopsis.
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Plant defense; Fungicide; Signal; Multigene family; Pyrrolidone carboxylic acid.
Pyrrolidone carboxylic acid.
29 POTENTIAL.
CHAIN 30 80 PROBABLE CYSTEINE-RICH
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InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
ProDom; PD002594; G Purchionin; 1.
SWART; SM00505; Knot1; 1.
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47
44
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NCBI_TaxID=3702;
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                                                                 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 AIGGCTAAGTITGCGTCCATCATCGCACTICTITTGCTGCTCTTGTTCTTTTGCTGCT 75
                                                                                                                                                                                                                                                                                                                                   Raphanus sativus (Radish).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Raphanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Broekaert W.F.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POSSESSES antifungal activity sensitive to inorganic cations (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYSTEINE-RICH ANTIFUNGAL PROTEIN PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
B5F667B6441818C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 4 precursor (AFP4).
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Matches:
Conservative:
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InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
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ProDom, PD002594, G Purothionin, 1.
SMART, SM00505, Knočl, 1.
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                                                                                                                                                                                                                             [6-OCT-2001 (Rel. 40, Created)
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Alignment Scores:

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HSSP; P30231; 1AYJ
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16-OCT-2001 (Rel. 40, Last sequence update)
18-OCT-2003 (Rel. 41, Last annotation update)
Probable cysteine-rich antifungal protein At2g26020 precursor (AFP).
AT2G26020 OR 19118.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. Columbia;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.E., Feldblyum T.V.,
Buell C.Y., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Buell C.R., Koronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
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    BY SIMILARITY.
2D0DAFB38E3B6321 CRC64;
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Matches:
Conservative:
Mismatches:
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       76
8518 MW;
                                                                                        1.54e-36
403.00
95.00%
88.75%
53.59%
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       54
80 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                              Similarity:
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Best Local Similarity
Query Match:
DB:
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0809<u>9</u>4;
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EMBL; AC004747; AAC31244.1; -. PIR; T02621; T02621.

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TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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16-CCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable cysteine-rich antifungal protein At2g26010 precursor (AFP).
AT2G26010 OR 119L18.18
Arabidopsis thallana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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STRAIN-cv. Columbia,
MEDLINE-2003487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Evijii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pari G., Van Aken S., Unayam L.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
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BY SIMILARITY.
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81B106058BAFFCC7 CRC64;
                Prodom; Profost; Audit:
Probom; Profost; Gamma-chionin; 1.
SWART; SM00505; Knoti; 1.
PROSITE; PS00940; GAWMA_THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family; Pyrrolidone carboxylic acid. BY SIMILARITY.
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InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
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400.00
93.75%
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Best Local Similarity:
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Pred. No.:
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thaliana (Mouse-ear cress).
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                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                         SEQUENCE FROM
          Arabidopsis
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                                                                                                                                                                  Raynal M.;
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EMBL;
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            PROBABLE CYSTEINE-RICH ANTIFUNGAL PROTEIN AT2626010.
PURCOLIDONE CARBOXYLIC ACID (BY SIMILARITY).
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01-APR-1993 (Rel. 25, Created)
15-DBC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 1 precursor (AFP1) (Anther-specific protein S18 homolog).
thaliana.";
Nature 402.761-768(1999).
--- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                  SUBCELLULAR LOCATION: Secreted (By similarity). SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                               PROSITE; PS00940; GAMMA_THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family;
Pyrrolidone carboxylic acid.
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InterPro; IPR008176; Gamma-thionin.
InterPro; IPR00814; Knoch.
Pfam; PP00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
SMART; SM00505; Knoch; 1...
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8580 MW;
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399.00
93.75%
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53.06%
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Best Local Similari
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DT 12-DEC-

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDININE-20106719; Pubmed=11130712;

MEDININE-2106719; Pubmed=11130712;

Theologis A. Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Mite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Medier E., Chan L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

A Langin-Hooper S., Lee A., Luros J.S., Marti R., Marziali A.,

Langin-Hooper S., Lee A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sahano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

W. Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

"Sequence and analysis of chromosome I of the plant Arabidopsis
Eukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99178804; PubMed=10080719; Williams R.W., Clark S.E., Meyercwitz E.M.; "Genetic and physical characterization of a region of Arabidopsis chromosome 1 containing the CatayATA1 gene."; Plant Mol. Biol. 39:171-176(1999).
                                                                                                                                                                                                                                                                                                   Σ.
                                                                                                                                                                                                                                                                                               Delseny
                                                                                                                                                                                                                                    STRAIN=cv. Columbia;
Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., De
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Forms oligomers in its native state.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=cv. Columbia; TISSUE=Seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Seed;
MEDLINE=93138130; PubMed=8422949;
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EMBL; Z29957; CAA82845.1; -.
EMBL; X91916; CAA63009.1; -.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 LeuGluAlaProMetValValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                              16 ATGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
peprantophyta; Magnoliophyta; endicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBL_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV. Naehan;
Sohn U., Lee C.M., Lee M.H., Kim J.H.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                         CYSTEINE-RICH ANTIFUNGAL PROTI-
PYRROLIDONE CARBOXYLIC ACID.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
C -> F (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cations (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                   C -> F (IN REF. 1).
99F34A8DA360441F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 3 precursor (AFP3).
            HSSP; P30231; 1AVJ.
InterPro; IPR00817; Gamma-thionin.
InterPro; IPR00817; Knot1.
Pfam; PF00304; Gamma-thionin; 1.
ProDom; P0002594; G Purothionin; 1.
SWART; SM00509; Knot1; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
PATCOlidone carboxylic acid.
1 29
                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                             80
30
80
65
74
76
33
8709 MW;
                                                                                                                                                                                                                                                                                                             7.11e-36
                                                                                                                                                                                                                                                                                                                          397.00
92.50%
87.50%
52.79%
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 PIR; F96787; F96787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                             Percent Similarity:
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Q39313;
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DISULFID
DISULFID
DISULFID
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CONFLICT
SEQUENCE
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DB:
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGAACATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 PheGluAlaProThrMetValGluAla---LysLeuCysGluArgSerSerGlyThrTrp 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 AIGGCIAAGTTIGCGICCAICAICGCACTICITITIGCIGCICTIGTICITITIGCIGCI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raphanus sativus (Radish).
Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: Possesses antifungal activity sensitive to inorganic cations (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Location family.
                                                                                                                                                                                                                                                          CYSTEINE-RICH ANTIFUNGAL PROTEIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed; Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Broekaert W.F.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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BY SIMILARITY.
3B5289FCFEA48936 CRC64;
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16-0CT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 3 precursor (AFP3).
                                                                                                              HSSP, P30231, 1AYJ.
InterPro: IPR008176; Gamma-thionin.
InterPro: IPR0086176; Gamma-thionin.
Prom: PF00304; Gamma-thionin; 1.
ProDom; PD002594; G Purothionin; 1.
PRORIT: PR00505; Knocll; 1.
PRORIT: PS00940; GAMMA_THIONIN; 1.
Plant defense; Pungicide; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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BY SIMILARITY
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                                                                                                                                                                                                                                           POTENTIAL.
                                                                                 EMBL; U59459; AAB03224.1; -. PIR; T07917; T07917.
                                                                                                                                                                                                                                                                     32 79
43 64
49 73
53 75
7A, 8555 MW;
                                                                                                                                                                                                                                                                                                                                                                                     1.34e-35
394.50
93.75%
91.25%
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AFP3_RAPSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetAlaLysPheAlaSerIleValAlaLeuLeuPheAlaAlaLeuValValPheAlaAla
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-203 (Rel. 41, Last annotation update)
28-FBB-203 (Rel. 41, Last annotation update)
28-FBB-203 (Rel. 41, Last annotation update)
Sinapls alba (White mustard) (Brassica hirta).
Sinapls alba (White mustard) (Brassica hirta).
Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
NCBI_TAXID=3728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYSTEINE-RICH ANTIFUNGAL PROTEIN 3.
BY SIMILARITY.
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BAFA80465DB48548 CRC64;
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Neumann G.M., Condron R., Polya G.M.;
"Purification and mass spectrometry-based sequencing of yellow mustard (Sinapis alba L.) 6 kDa proteins. Identification as
                                                                                                                                                                                                                                     EMBL, X97319; CAA65984.1; -...
PIR; T10243; T10243.
HSSP, P30231; 1AVJ.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR008176; Gamma-thionin.
Prom; PF00304; Gamma-thionin, 1.
ProDom; PF000594; G Purcthionin, 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
PLANT defense; Fungicide; Signal; Multigene family.
SIGNAL
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AA.
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79
79
73
75
8479 MW;
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393.50
95.00%
90.00%
52.33%
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43
53
AA;
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TISSUE=Seed;
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222
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                                                                                                                                                                   STRUCTURE BY NMR.
MEDLINE=98300344; PubMed=9636715;
MEDLINE=98300344; PubMed=9636715;
Fant F., Vranken W.F., Broekaert W.F., Borremans F.A.M.;
Fant F., Vranken W.F., Broekaert W.F., Borremans F.A.M.;
"Determination of the three-dimensional solution structure of Raphanus activus antifungal protein 1 by 1H NMR.";
J. Mol. Biol. 279:257-270(1998).
-I. FUNCTION: Possesses antifungal activity sensitive to inorganic
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                                                                                                                                                                                                                                                                                                                                                              InterPro; LPRUJOSA*; ANDOLI.
PERM, PROBLO34, Gamma-thionin; 1.
SYARI, SM00505; KnoEl; I.
PROSITE; PS00940; GAMMA, THTONIN; 1.
PROSITE; PS00940; GAMMA, THTONIN; 1.
PROSITE; PS00940; GAMMA, THTONIN; 1.
PROFILED PROFILES (Pungicide; 3D-structure; Pyrrolidone carboxylic acid.
WAND PROFILES (PUNGICIDE) PYRROLIDONE CARBOXYLIC ACID.
                                                                   MEDLINE=93138130; PubMed=8422949;
Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
"A new family of basic cysteine-rich plant antifungal proteins from
Brassicaceae species."
                                                                                                                                                                                                                                                                       770990E72DD1C469 CRC64;
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Mismatches:
Indels:
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2010 (Rel. 41, Last annotation update)
Streine-rich antifungal protein 2A (APP2A) (M2 Sinapis alba (White mustard) (Brassica hirta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
antifungal proteins.";
Int. J. Pept. Protein Res. 47:437-446(1996)
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Matches:
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                                                                                                                                             FEBS Lett. 316:233-240(1993).
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309.00
100.00%
100.00%
41.09%
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36
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47
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Best Local Similarity:
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AA;
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AF2A SINAL
1D AF2A SINAL
AC P30232;
DT 01-APR-1993
DT 01-OCT-1996
DT 28-FEB-2090
DE Cysteine-ricl
OS Sinapis alba
                                          SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
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DISULFID
STRAND
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103 CAGAAGTIGIGCGAAAGGCCAAGIGGGACAIGGICAGGAGTCIGIGGAAACAAIAACGCA 162
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Sinapis.
                                                                                                                                                                                                                                                               MEDLINE-93138130; PubMed-8422949;
Perras F. N.G., Torrekens S., van Leuven F., Osborn R.W.,
Vanderleyden J., Cammue B.P.A., Broekaart W.F.;
"A new family of basic cysteine-rich plant antifungal proteins from
Basslaceaes species.";
FEBS Lett. 316:233-24(11993).
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBUNIT: Forms oligomers in its native state.
-1- MASS SPECTROMETRY: WW-5705; WW ERR-0.8; METHOD=Electrospray.
-1- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                MEDLINE=56433791; PubMed=8836771;
Neumann G.M., Condron R., Polya G.M.;
"Purification and mass spectrometry-based sequencing of yellow
mustard (Sinapis alba L.) 6 KDa proteins. Identification as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00940; GAMMA_THIONIN; 1.
Fungicide; Phosphorylation; Pyrrolidone carboxylic acid.
MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.
MOD_RES 8 PHOSPHORYLATION (BY CDFK).
DISULPID 4 51 BY CTUTTONIC CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
1C7F50E72DC945B1 CRC64;
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1 0
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FBD-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 2B (AFP2B) (M2B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
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InterPro; IPRO08176; Gamma-thionin.
InterPro; IPR008176; Gamma-thionin.
Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
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100.00%
96.08%
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SEQUENCE OF 1-26.
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Best Local Similarity:
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Q10989;
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ID AF2B_SI
AC 010989,
DT 01-0CT-
DT 28-FEB-
DE CYSteir
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160 GCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTC 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 28, Last sequence update)
01-REB-1994 (Rel. 28, Last sequence update)
01-REB-1994 (Rel. 28, Last annotation update)
Cysteine-rich antifungal protein 1 (AFP1) (Fragment).
Brassica rapa (Turnip).
Brassica rapa (Turnip).
Sparmatophyte, Magnoliophyte; endicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
NCBL_TAXID=51350;
                                                                                                                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
                                                                                                                                                                           antifungal proteins.";
Int. J. Pept. Protein Res. 47:437-446(1996).
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                       -!- SUBUNIT: Forms oligomers in its native state.
-!- MASS SPECTROMETRY: MW-5840; MW_ERR=1.2; METHOD=Electrospray.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                   TIŜSUE=Seed;
MEDLINE=S6433791; PubMed=8836771;
Neumann G.M., Condron R., Polya G.M.;
"Purification and mass spectrometry-based sequencing of yellow
mustard (Sinapis alba L.) 6 kDa proteins. Identification as
                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
A060FCBC13A8D1FB CRC64;
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20
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Matches:
Conservative:
Mismatches:
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Sinapis alba (White mustard) (Brassica hirta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 AA
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Fungicide, Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
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InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                                                                                                                                                                                                                                                                                            Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G Purothionin; 1.
SMART; SM00505; Knot1; 1.
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TISSUE=Seed;
MEDLINE=93138130; PubMed=8422949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5856 MW;
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84.62%
76.92%
31.05%
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Best Local Similarity:
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P30227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 CAGAAGTIGIGCGAAAGGCCAAGIGGGACAIGGICAGGAGICIGIGGAAACAAIAACGCA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 29, Last sequence update)
01-AUG-1994 (Rel. 29, Last annotation update)
01-JUN-1994 (Rel. 29, Last annotation update)
Anther-specific protein SF18 precursor (Fragment).
Helianthus annuus (Common sunflower).
Fukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
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STRAIN=cv. HA401B / Cargill; TISSUE=Anther;
MEDLINE=9133702; Pubmed=2102380;
Domon C., Evrard J.-L., Herdenberger F., Pillay'D.T.N., Steinmetz A.;
"Nucleotide sequence of two anther-specific cDNAs from sunflower
(Helianthus annus L.).";
Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W., Vanderleyden J., Cammue B.P.A., Broekaert W.F.; An ew family of basic cysteine-rich plant antifungal proteins from Brassicaceae species."

FEBS Lett. 316:233-240(1993).

-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                -!- SUBUNIT:
-- SIMILARITY: Belongs to the plant defensin family.
-!- SIMILARITY: Belongs to the plant defensin family.
-!- SIMILARITY: Belongs to the plant defensin family.
HSP, P30891; 1AVJ.
INTER-PRO; 1R00816; Gamma-thionin.
Pfam; PF00304; Gamma-thionin; 1.
PRODOM; P5002594; G_PUTCHIONIN; 1.
PROSITE; P500940; GAMMA.
PNDINIT; PS00940; GAMMA.
PNDINIT; PS00940; GAMMA.
PNDINIT; PS00940; GAMMA.
-- PARROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                              4C85BD9C611D4A9E CRC64;
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 TGCAAGAATCAGTGCATTAAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 CysLysAsnGlnCyslleAsn 27
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SEQUENCE 27 AA; 2925 MW;
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100.00%
100.00%
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Best Local Similarity:
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                                                                                                          cations.
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106 AAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGCAGTCTGTGGAAACAATAACGCATGC 165
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36 AspLysArgCysIleAspTrpGluGlyAlaLysHisGlyAlaCy8HisGlnArgGluAla 55
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MEDLINSE-91130; PubMed=8422949;
TEXTES F.R.G., TOTTERERS S., van Leuven F., Osborn R.W.,
Vanderleyden J., Cammue B.P.A., Broekeert W.F.;
Vanderleyden J., Cammue B.P.A., Broekeert W.F.;
A new family of basic cysteine-rich plant antifungal proteins from
Brasslacaceae species.";
FBBS Lett. 316:233-240(1993).
-!- FMDVTION: Possesses some antifungal activity sensitive to
inorganic cations and antibacterial activity against B.megaterium.
-!- SUBUNIT: Forms oligomers in its native state.
-!- SINTLARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=51350;
                                                                                                                                                                                                                                                                                                                                                                                ANTHER-SPECIFIC PROTEIN SF18.
GAMMA-THIONIN LIKE DOMAIN.
PROLINE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27A9CF4633ADA02B CRC64;
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01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Cysteine-rich antifungal protein 2 (AFP2) (Fragment).
Brassica rapa (Turnip).
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                  ProDom, PD002594, G Purcthionin, 1. SMART; SM05055, Knotl; 1. SM0501E, PS00940, GANWA_THIONIN; 1. Signal; Cell wall. 1 1
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                                                                                                       HSSP, P30231, 1AYJ.
InterPro; IPR008176, Gamma-thionin.
InterPro; IPR00314, Knot1.
Pfam; PP00304; Gamma-thionin; 1.
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                                                      EMBL; X53375; CAA37455.1; -. PIR; S12246; S12246.
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HSSP; P30231; 1AYJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 AA;
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AFP2_BRARA
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Length:
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Mismatches:
Indels:
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Best Local Similarity: 9
Query Match:
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US-10-006-252A-19 (1-414) x AFP2\_BRARA (1-27)

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Search completed: May 11, 2004, 17:03:07 Job time : 29 secs

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Q810h2 mus musculu
Q9nap6 caenorhabdi
Q94az8 arabidopsis
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094IN7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Defensin precursor.
Defensin precursor.
Brassica oleracea (Cauliflower).
Brassica oleracea (Cauliflower).
Brassica oleracea (Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; NCBL TAXID=3712;
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Q39807
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Q810H2
Q9NAP6
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P82756
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Q9FWR6
Q8LSM8
Q40128
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Q8GTL2
Q8GTM0
Q40779
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Q9SEM4
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                                                                           (without alignments) 6371.929 Million cell updates/sec
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                                                                 May 11, 2004, 16:58:28 ; Search time 41 Seconds
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                             protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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sp_unclassified:*
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1: sp_archea:*
2: sp_bacteria:*
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4: sp_human:*
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Fgapop 6.0 , Fgapext
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Best Local Similarity:
Query Match:
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MEDINE-21071227; PubMed=11204773;
Saitoh H., Kiba A., Nishihara M., Yamamura S., Suzuki K., Terauchi R.;
Saitoh H., Kiba A., Nishihara M., Yamamura S., Suzuki K., Terauchi R.;
Saitoh H., Kiba A., Nishihara M., Yamamura S., Suzuki K., Terauchi R.;
Production of antimicrobal defensin in Nicotiana benthamiana with a potato virus X vector.";
Mol. Plant Wicrobe Interact. 14:111-115(2001).
HSSP: P30231; 1AVJ.
G0; G0:0003793; Fdefense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
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Bukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Eutrema.
NCBI_TaxID=75806;
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CF2F10ADD38FC87A CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Gamma-thionin1 precursor.
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Pfam; PF00304; Gamma-chionin; 1.
Probom; PD002594; G Purchionin; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
                                                                                                                                                                                                                                                                                                                                              (1-80)
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          SMART; SM00505; Knotl; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
                                                                                                                                                                                                                                                                                                                                              US-10-006-252A-19 (1-414) x Q94IN7
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407.00
96.25%
90.00%
54.12%
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                                                                               1 29
80 AA; 8740 MW;
                                                                                                                                                                   5.6e-41
421.00
96.25%
93.75%
55.98%
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Score:
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                                                                                                                                                                                                                           Percent Similarity:
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                                                                                                      SEQUENCE
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SIGNAL
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255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                        135
                                                                                                                                                                              TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
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                      76 TICGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG
                                                                                                                 21 PheGlualaproSerMetValGlualaGlnLysLeuCysGluLysSerSerGlyThrTrp
                                                                                                                                                                                                            41 SerGlyValCySGlyAsnAsnAsnAlaCySLySAsnGlnCys11eAsnLeuGluGlyAla
                                                                                                                                                                                                                                                                         CGACATGGAATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage). Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ryang S. H., Chung S.-Y., Park Y.-S., Cho T.-J.; "Characterization of Chinese cabbage genes induced by Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          syringae pv. tomato...'
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS28186; AAN23105.1; -..
GO; GO: 0003793; Fidefense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR008176; Gamma-thionin.
Pfam; PF00304; Gamma-thionin, 1.
Profon; P000594; G Purchionin; 1.
Profon; P000595; Knotl; 1.
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80 AA; 8864 MW; 485CC5A95905E92C CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches:
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ArgHisGlySerCysAsnTyrValPheProTyrHisArgCysIleCysTyrPheProCys 80
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01-MAR-2003 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Antifungal protein-like.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta; eudicotyledons, core eudicots, rosids, NCBL TAXID=3702;
NCBL_TAXID=3702;
                                                                                                                                                                                                                         STRAIN-Columbia;
MEDLINE-29939451; PubMed=10470850;
Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
Miyajima N., Tabata S.;
Structural analysis of Arabidopsis thaliana chromosome 5. IX.
Sequence features of the regions of 1,011,550 bp covered by sevent and TAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative antifungal protein (Cysteine-rich antifungal protein,
                                                                                                                                                                                                                                                                                                                                                                 protein activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SMEAL! SMOSSO, ALCOL, A.
PROSITE; PS00940; GAMMA_THIONIN; 1.
SEQUENCE 80 AA; 8550 WW; 44E1F6D8452AC76E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
7 7 1
0 0
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Matches:
Conservative:
Mismatches:
Indels:
                                                        80 AA
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T24C10.12 OR F14C21.57.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003614, Knot1.
Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G Purothionin; 1.
SMART; SM00505; Knot1; 1.
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                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                          GO; GO:0003793; F:defense/immunity
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
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EMBL; AB017065; BAB09150.1; -.
HSSP; P30231; 1AYJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.01e-38
398.00
93.75%
88.75%
52.93%
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                                                   PRELIMINARY;
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Best Local Similarity:
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01-MAR-2001 (
01-MAR-2001 (
01-OCT-2003 (
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Q9F231
ID Q9F2
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SEQUENCE Columbia,

X. MEDIANE=2016719; Pubmed=11130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Theologis A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Buchler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Crasay T.H., Dewar K.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Kim C.J., Noo H.L., Kremeneskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Link X., Liu S.A., Luros J.S., Maiti R., Marziali A.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Sann H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Utterback T., Van Aken S., Vasberg M., Vysotskaia V.S., Walker M.,

RA Will Sequence and analysis of chromosome I of the plant Arabidopsis
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υποιγοτα; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
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| SerGlyArgCysValAsnAspTyrGlnCysArgAspHisCyslleAsnAsnAspArgGly
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                                                                                                                                                                            Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A., Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M., Lenz C., Liu A., Liu S., Wukharsky N., Pham P., Sakano H., Shinn P., Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein activity, IEA.
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9139 MW; BEFBF4ACA7974071 CRC64;
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Mismatches:
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ProDom; PD002594; G_Purothionin; 1.
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67.90%
49.38%
27.53%
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PD002594; G_FU
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Best Local Similarity:
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                                                                                                                                                      SEQUENCE
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208 IGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
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                                                                                                                                             O9FWR6;
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                                                                                  RESULT 7
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Yamada K., Barbh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,

Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,

Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

A carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

Miranda M., Narusaka M., Ngiyah M., Palm C.J., Sakurai J. Satou M.,

Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

A raboldopsis Open Reading Frame (ORF) Clones.";

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

BMBL, ANG63931, AAL362891;

LI Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

R PRED, AY114039; AAM45086.1;

R PROSTITS; PS003049; Gamma-thionin;

R Probom, PD002594 Gamma-thionin;

R PROSTITE; PS00340; GAMMA THIONIN;

R PROSTITE; PS00409, GAMMA THIONIN;

R PROSTITE; PS0040940; GAMMA THIONIN;

R PROSTITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 ACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 GGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 GCGTCCATCATCGACTTCTTTTGCTGCTCTTGTTCTTTTTGCTGCTTTTCGAAGCACCA 87
                                                                                                                                                                                                                                                                                                                                                                                                                      Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Theologis A.,
                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Full Length cDNA of gene At1g19610 (GI:15223595).";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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0 0 35
0 0 0
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Last annotation update)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                    Created)
                                                                                                                                                                                01-WAR-2002 (TrEMBLrel. 20, Cres
01-WAR-2002 (TrEMBLrel. 20, Last
01-0CT-2003 (TrEMBLrel. 25, Last
Putative defensin AMPI protein.
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181.00
53.95%
40.79%
24.07%
                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                       253 TGT 255
                                                               80 Cys 80
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DB:
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106 AAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 165
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EMBL; ACC24609; AAPS9402.1; --

EMBL; ACC24609; AAPS9402.1; --

EMBL; ACC34609; ARPS9402.1; --

END; GO:0003793; F.defense/immunity protein activity; IEA.

InterPro; IPRO08176; Gamma-thionin.

Probom; PD002594; Gamma-thionin; 1.

Probom; PD002594; Gamma-thionin; 1.

PROSTER; PS00940; Gamma-thionin; 1.

PROSTER; PS00940; Gamma-thionin; 1.

PROSTER; PS00940; Gamma-thionin; 1.

PROSTER; PS00940; Gamma-thionin; 1.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
campanulids, Asterales, Asteraceae, Asteroideae, Heliantheae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
63 CysHisalaGlnPheProGlyPheAlaCysPheCysTyrPheAsnCys 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
25
7
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01-0cT-2002 (TrEMBLrel. 22, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                 56 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyPheAlaCysPheCysTyrPheAsnCys 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
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                                                                                                                                                 PRT;
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164.00
64.00%
50.00%
21.81%
                                                                                                                                                 PRELIMINARY;
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Best Local Similarity:
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Percent Similarity:
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01-JUN-2003
                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                   16
                                                                                                                                                                                                                                                                                                                                                                                                                                           94
                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                Query Match:
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SIGNAL
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No.:
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Q84ZX5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 AGTIGIGCGAAAGGCCAAGIGGGACAIGGICAGGAGICIGIGGAAACAAIAACGCAIGCA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 --LeucysGluLysAlaSerGlnThrTrpSerGlyThrCysGlyLysThrLysHisCysA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum (Tomato).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
Lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 AGAATCAGTGCATTAAACCTTGAAAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAG
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C STRAIN-WITH 1954, TISSUB-Pistil;

MEDLINE-95375233; PubMed=7647301;

Milligan S.B., Gasser C.S.;

"Nature and regulation of pistil-expressed genes in tomato.";

I Nature and regulation of pistil-expressed genes in tomato.";

I Plank Mol. Biol. 28.691-711(1995).

R EMBL; U20591; AAA80496.1; -.

R PIR; S57809; S57809.

R Of GO:0003793; F:defense/immunity protein activity; IEA.

R InterPro; IPR003176; Gamma-thionin.

R InterPro; IPR003614; Knoct.

R Probom; PF00364; Gamma-thionin; 1.

R SYAAR; SM00505; Knocli; 1.
                                                                                       Hu X., Bidney D., Duvick J., Yalpani N., Crasta O., Folkerts O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NoV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-12003 (TrEMBLrel. 25, Last annotation update)
Flower-specific gamma-thionin-like protein/acidic protein
                                                                                                                            "Oxalate oxidase confers Sclerotinia resistance."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF364865, AAM27941.; GO; GO:0003793; F:defense/immunity protein activity; IEA. InterPro; IPR008176; Gamma-thionin. InterPro; IPR008176; Gamma-thionin. Prodom; PP00304; Gamma-thionin. 1.
                                                                                                                                                                                                                                                                                                                          SMART; SM00505; Knot1; 1.
SEQUENCE 108 AA; 11866 MW; 631ECD8F02F21AD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     108
33
9
13
13
13
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 105
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                                                                                                                                                                                                                                                                                                                                                                                                                3.2e-09
153.50
59.15%
46.48%
20.41%
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                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
Query Match:
                     NCBI_TaxID=4232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
  Helianthus
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                               55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73
                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annocation update)
Major pollen allergen Art v | precursor and allergen Art v |
Artemisia vulgaris (Mugwort).
Bukaryora, Viridiplancae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudiocyyledons, core eudicots; asterids, campanulids; Asterales, Asteraceae, Asteroideae, Anthemideae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 ThrGlyGlyHisCysSerLysLeu-----GlnArgLysCysLeuCysThrLysProCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Himly M., Jahn-Schmid B., Dedic A., Kelemen P., Wopfner N.,
Altmann F., van Ree R., Briza P., Richter K., Ebner C., Ferreira F.;
"Art v 1, the major allergen of mugwort pollen, is a modular
glycoprotein with a defensin-like and a hydroxyproline-rich domain.";
PASEB J. 17:106-108(2003).
EMBL, AF493943; AA024900.1;
GO; GO:0003193; F:defense/immunity protein activity; IEA.
InterPro; IPR008164; Knotl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 ProdlyLeuCysPheMetAspSerSerCysArgLysTyrCyslleLys---GluLysPhe
                                                                                                                                                                                                                                                                                                                                 ATGCCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAJOR POLLEN ALLERGEN ART V 1.
745249C89919F316 CRC64;
POTENTIAL.
GAMMA-THIONIN-LIKE PROTEIN.
ACIDIC PROTEIN.
ADC987ECB620E814 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                      US-10-006-252A-19 (1-414) x Q40128 (1-105)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Pollen;
MEDLINE=22409970; PubMed=12475905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00304; Gamma-thionin; 1. SMART; SM00505; Knot1; 1.
                                                                  11914 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13404 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.49e-07
139.50
50.00%
                                                                                                                                  8.48e-08
                                                                                                                                                    141.50
58.54%
37.80%
18.82%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
132
    26
105
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25
132 AA;
    1
27 ,
74 1
105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 TAATTT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 ValPhe 75
                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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99

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AN 11 To Schirra H.J., Scanlon M.J., Anderson M.A., Craik D.J.;
An Lay F.T., Schirra H.J., Scanlon M.J., Anderson M.A., Craik D.J.;
An Lay F.T., Schirra H.J., Scanlon M.J., Anderson M.A., Craik D.J.;
RT "The three-dimensional solution structure of NaD1, a new floral
RT defensin from Nicotiana alata and its application to a homology model
RT of the crop defense protein alfAPP.";
DR GG.GO:0003793; F.defense/immunity protein activity; IEA.
DR GO, GO:0003793; F.defense/immunity protein activity; IEA.
DR RTC-PRO03614; Gamma-thionin.
DR ProDom; PD002594; G_Purothionin; 1.
DR PRODOM; PRO0365; Knotl: 1.
DR PROSTIE; PS00940; GAWMA_THIONIN; 1.
DR PROSTIE; PS00940; GAWMA_THIONIN; 1.
DR PROSTIE; PS00940; GAWMA_THIONIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NADI.

NACI.

NICOLIAna alata (Winged tobacco) (Persian tobacco).

Bukaryota; Viridiplantae; Streptophyra; Embryophyra; Tracheophyra;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetalaArgSerLeuCysPheMetAlaPheAlaIleLeuAlaMetMetLeuPheValAla
                                                       48 AlaSerArgAshAsnCysLysAsnValCys---GlnThrGluGlyPheProSerGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
148 GGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCT
                                                                                                                        TGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                               FLOWER-SPECIFIC DEFENSIN.
DA7F41736CEE6AC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last seq
(TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flower-specific defensin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN 26 72 F.
SEQUENCE 105 AA; 11722 MW;
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53.66%
32.93%
15.43%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 TAATTT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 ValPhe 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4087;
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01-OCT-2003
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                                                                                                                           208
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                                                                                                                                                                                                                                                                                                               OBGTMO
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                                                                                                                                                                                                                                          RESULT 12
Q8GTM0
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ID 04
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                                                                                                                                                                                                                                                                                                                                                                                                                                       133 TGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAA 192
                                                                                                                                                                                                                                                                                                               73 GCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 ATGGTGGAAGCACAG---AAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGT 147
                                                                                                                                                                                      16 AIGGCIAAGITIGCGTCCAICATC - - GCACTICTITITGCIGCTCTTGTTCTTTTGCT 72
                                                                                                                                                                                                                                                                                                                                                                      21 GluMetGluAla-----AlaGlySerLySLeuCySGluLySThrSerLySThr 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----HisiysArgGluAlaGlyLysGlu 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 TCCATCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTTGCTGCTTTTCGAAGCACCAACA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerArgLeuSerAlaLeuPheLeuValLeuValIleSerIleGlyMetMetGln 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The putative gymnosperm plant defensin (SPII) accumulates after seed germination and a related SPIIB cDNA is found in needles."; Submitted (SEP-2002) to the EMEL/GenBank/DDBJ databases.

EMEL, AF548021; AAN406881. - GO, GO:0003793; F:defense/immunity protein activity; IEA.

InterPro; IPR008176; Gamma-thionin.

InterPro; IPR00304; Gamma-thionin, 1.

ProDom; PD002594; G Purothionin, 1.

ProDom; PD002594; G Purothionin; 1.

PROSITE; PS00546; GAMMA-THIONIN; 1.

SEQUENCE 83 AA; 8888 MW; E45BF9E6IB9AA3D2 CRC64;
                                                                                                                                                                                                                             01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLRel. 23, Last an
         139
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Mismatches:
Indels:
      Mismatches:
Indels:
Gaps:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---TGTATCTGCTACTTTCCTTGT 255
                                                                                                                               US-10-006-252A-19 (1-414) x Q84ZX5 (1-132)
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| AlaGlnHisGlyAlaCys-----
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118.00
51.32%
34.21%
      38.64%
18.55%
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      Best Local Similarity:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sharma P., Linneborg A.; Isolation and characterization of a cDNA encoding a gamma-thionin-lise protein from roots of Norway spruce."; Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.

BME1, X91487; CAA62761.1; -...

PIR, T14866; T14866.

HSSP, P41964; IMYN.

CO, GO.0003793; F. defense/immunity protein activity; IEA.

InterPro: IPR003794; Knot1.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
NCBI_TaxID=157791;
                    SEQUENCE FROM N.A. MCCollum T.G., Mayer R.T.; McKendree W.L., Doostdar H., McCollum T.G., Mayer R.T.; "cDNA cloning and expression of a gene (Accession No. 297064) from Citrus paradisi roots similar to bacterial YRN1 and HEAHIO proteins and an MRNA from Brassica oleracea that is wound and dark inducible (PGR97-127).";
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to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
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EMBL, AB005266; BAA21114.1; -.

GO, GO:0003793; F:defense/immunity protein activity;
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knoti.
Pfam; PF00304; Gamma-thionin, 1.
Probom; PD002594; G Purothionin; 1.
SWART; SM00505; Knoti; 1.

PROSITE; P$00940; GAMWA THIONIN; 1.

SEQUENCE 105 AA; 11635 MW; B7C586CB8DB565DF CRC64
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InterPro; IPR003614; Knot1.
Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
SMART; SM00505; Knot1; 1.
SEQUENCE 75 AA; 8631 MW; 6AC570E92D88013E CRC64;
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Conservative:
Mismatches:
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112.00
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211 AACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTCCTTGT 255 

Search completed: May 11, 2004, 17:04:29 Job time: 43 secs

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OM nucleic - nucleic search, using sw model
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Total number of hits satisfying chosen parameters: 6940544
Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
Database : GenEmbl:\*
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AUTHORS	Bro	ekaert,	13. F1.	Jamm	le, B. P. A., Ter		G., Vanderl	rleyden, J.,
	qso	orn, R.	۸. and ا	sees	, s.B.			

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Dubock, A.C., Fowell, K.A. and Rees, S.B.
MINIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
Patent: MO 9416076-A 37 21-JUL-1994;
ZENECA LTD (GB)
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/organism="Raphanus sativus"
BIOCIDAL PROTEINS
Patent: WO 9305153-A 33 18-MAR-1993;
ICI PLC (GB)
                                                                                     /mol_type="unassigned DNA"
/db_xref="taxon:3726"
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Patent: W0 9721814-A 19 19-JUN-1997,
ZENECA LTD (GB)
Other publication AU 1105397 19970703.
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 19 from Patent W09721814.
A63404
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ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES

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RESULT 4 AR050153

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RESULT 5
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PAT 07-0CT-1996
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        1 (bases 1 to 414)
Broekaert,W.F., Cammue,B.F.A., Osborn,R.W., Rees,S.B.,
Terras,F.R.G. and Vanderleyden,J.
Blocidal proteins
Patent: US 6187904-A 48 13-FEB-2001;
Location/Qualifiers
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Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Terras, P.R.G. and Vanderleyden, J.
Blocidal proteins
Patent: US 5538525-A 48 23-JUL-1996;
Location/Qualifiers
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Sequence 48 from patent US 5538525.
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Brockeert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Blocidal proteins
Patent: US 5824869-A 48 20-OCT-1998;
Location/Qualifiers
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100.0%; Score 414; DB 6; Length 414;
Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 414; Conservative 0; Mismatches 0; Indels
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Sequence 48 from patent US 5824869.
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AR050153.1 GI:5972145
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/mol_type="unassigned DNA"
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Sequence 48 from patent US 6187904.
AR130272
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De Samblanx, G.Wirina., Broekaert, W.Frans. and Rees, S.Bronwen.
Antifungal proteins
Patent: US 6372888-A 19 16-APR-2002;
Location/Qualifiers
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/mol_type="unassigned DNA"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
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                                                                                                                                                                                                                                                                                                                                    Unclassified.

1 (bases 1 to 414)

1 (bases 1 to 414)

Sijtema, L., Welchen, R.H., Puijk, W.C., Schapper, W.M.M.,

Sijtema, L., Welchen, R.H., Puijk, W.C., Schapper, W.M.M.,

Antifungal peptides and composition thereof

Batent: US 6605698-A 45 12-AUG-2003;

Location/Qualifiers
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                                                                                                                                                                          linear
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Sequence 45 from patent US 6605698.
AR374914
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/organism="unknown"
/mol_type="genomic DNA"
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269 TATTICCCTIGITIAATICCATAAACICTICGGIGGITAATAGIGIGGGATTITACATAT 328
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/function="antifungal, fungistatic"
/function="antifungal, fungistatic"
/functe="Evidence for antifungal activity: Analysis of two novel classes of antifungal activity from radish (Raphanus sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="antifungal protein 1 preprotein"
|protein id="AAA6942".1"
| protein id="AAA6932" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322" | 1.009322"
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      1 (sites)
Terras,F.R.G., Eggermont,K., Kovaleva,V., Raikhel,N.V.,
Osborn,R.W., Kester,A., Rees,S.B., Torrekens,S., Van Leuven,F.,
Vanderleyden,J., Cammue,B.P.A. and Broekaert,W.F.
Small cysteine-rich antifungal proteins from radish: their role in
                                                                                                                                                                                                                                                             Direct Submission
Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
of Genetics, Applied Biological Sciences, W. De Croylaan 42,
Heverlee, Belgium, B-3001
On Feb 9, 1995 this sequence version replaced gi:609321.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                forganism="Raphanus sativus"
mol type="mRNA"
strain="ronde rode kleine witpunt"
db_xref="taxon:3726"
tissue_type="seed"
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/note="18 A nucleotides"
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Chem. 267, 15301-15309"
/citation=[1]
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2 (bases 1 to 395)
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102. 254
/gene="Rs-AFP1"
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C12N15/09,A01H5/00,A01N65/00,C07K14/415,C12N1/21,C12N5/10// PC (C12N15/09,C12R1:91), (C12N1/21,C12R1:91), (C12N5/10,C12R1:91), PC
                                                                                                                                                                                                                                                                                                              E34290 10 DNA linear PAT 31-JAN-2002 based and plasmid constructed by ligating antibacterial protein gene DNA with vector DNA, transformant microorganism and transformant plant containing the same and antibacterial protein.
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362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phage and plasmid constructed by ligating antibacterial protein gene DNA with vector DNA, transformant microorganism and transformant plant containing the same and antibacterial protein TOYAMA PREF
OS Raphanus sativus L.
PN JP 2000116379-A/1
PN JP 2000116379-A/1
PN JP 2000116379-A/1
PN JP 2000116379-A/1
PN JP 2000116379-A/1
PN JP 2000116379-A/1
PN JP 2000116379-A/1
PN JP 2000116379-A/1
PN JP 2000116379-A/1
PN JP 2000116379-A/1
PN JP 2000116379-A/1
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   303 AAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 rragragricardecraagringcriccarcardrecricicricorrecriere
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PC C12N5/00, (C12N5/00,C12R1:91), (C12N5/00,C12R1:91)
FH Key Location/Qualifiers
1. .449
FT source 1. .449
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Pred. No. 3e-50;
                                                                                                                                              362 IGGIICGGIIATACAAAIAAAGIIITAIICACCA 395
                                                                                                            363 TGGTTCGGTTATACAATAAAGTTTTATTCACCA 396
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    449
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/db_xref="taxon:32644"

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E34290.1 GI:18624295
JP 2000116379-A/1.
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Best Local Similarity 81.0%;
Matches 333; Conservative
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61 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
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Brockaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: US 6187904-A 58 13-F3B-2001;
Location/Qualifiers
                                                                             Length 288;
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                                                                         61.4%; Score 254.2; DB 6;
ilarity 98.8%; Pred. No. 4.9e-50;
Conservative 0; Mismatches 3:
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Sequence 58 from patent US 6187904.
AR130280.1 GI:14118177
1. .288
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/mol_type="unassigned DNA"
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Best Local Similarity 98.8
Matches 256; Conservative
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                       329 AATTAATAAGTTTGTGTCACTATTTATTAGTGACTTTATGACAGGTGTGCCAGGTATGTTTA 388
     301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATG-TTA 359
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Dubock,A.C., Powell,K.A. and Rees,S.B.
ANTIMICROBIAL-PROTBIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
PATENT: WO 9416076-A 41 21-JUL-1994;
ZENECA LTD (GB)
                                                                 389 TGTTGGTTTGGTAATATAAAAAAGTTTACGGATATAATAAGATGATAA 439
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Local Similarity 98.8%; Pred. No. 4.9e-50;
les 256; Conservative 0; Mismatches 3; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GITITATIAGEGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTT
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Other publication AU 5820494 940815.
Location/Qualifiers
1. 288
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Sequence 58 from patent US 5824869.
AR050161. GI:5972153
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Sequence 41 from Patent WO9416076.
A39553
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AR050161
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PAT 16-MAY-2001

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/ground: antifungal protein 2"
/function="antifungal, fungistatic"
/function="antifungal, fungistatic"
/functe="Evidence for antifungal activity: Analysis of two
novel classes of antifungal proteins from radish (Raphanus
sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
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/db protein id="09320"
/db protein id="MAKEASIIVLEVALVVPAAFEEPTMVEAQKLCORPSGTWSGVCGNNNACKNQCIRLEKARHGSCNYVFPAHKCICYFPC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 TACTTTCCTTGTTAATT-TATCGCAAACTCTTTGGTGAATAGTTT--TTATGTAATTTAC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 Tragraguearcardecraagirrecricrarcarrercricricerrecristic
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of Genetics, Applied Biological Sciences, W. Heverlee, Belgium, B-3001
Location/Qualifiers
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/function="antifungal, fungistatic"
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Chem. 267, 15301-15309"
/citation=[1]
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/gene="Rs-AFP2"
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ilarity 80.4%;
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Direct Submission
Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
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Brockaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: US 5538525-A 58 23-JUL-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cch 61.4%; Score 254.2; DB 6; Length 288; al Similarity 98.8%; Pred. No. 4.9e-50; 256; Conservative 0; Mismatches 3; Indels 0
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                                                                                                   123736 28 from patent US 5538525.
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4.

Length 457;

Score 249.8; DB 8; Length Pred. No. 5.1e-49; 0; Mismatches 76; Indels

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Search completed: May 13, 2004, 10:11:02 Job time : 1790 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

May 13, 2004, 08:35:18 , Search time 352 Seconds (without alignments) 4996.460 Million cell updates/sec Run on:

US-10-006-252A-19 414 Title: Perfect score:

Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

3373863 segs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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11: geneseqn1980s:\*
2: geneseqn1980s:\*
3: geneseqn2000s:\*
4: geneseqn2001s:\*
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24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity. AAQ38650 standard; DNA; 414 BP. (revised)
(first entry) Rs-AFP1 CDNA. 25-MAR-2003 07-JUL-1993 AAQ38650; RESULT 1 AAQ38650 

Location/Qualifiers 16. .256 /\*tag= a Raphanus sativus.

WO9305153-A1

92WO-GB001570. 27-AUG-1992; 18-MAR-1993

91GB-00018523. 92GB-00003038. 92GB-00013526. 29-AUG-1991; 13-FEB-1992; 25-JUN-1992;

(ICIL ) IMPERIAL CHEM IND PLC.

Terras FRG; Rees SB, Cammue BPA, Osborn RW, Broekaert WF, ( Vanderleyden J;

WPI; 1993-100978/12.

Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial diseases.

Example 21; Fig 35; 110pp; English.

This cDNA represents the sequence of Rs-AFP1 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for

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screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 123bp product, which was further reamplified with the same primers and digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII cDNA library by in situ plaque hybridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage then into the pBluescript phagemid form with the aid of helper phage then. Size compared by agarose gel electrophoresis. Four clones had insert sizes of approx. 400bp the others between 250-300bp. The inserts of the 4 largest clones were then sequenced and found to differ only in the length of their 5 and 3 'UTK's. The longest sequence is given here.
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Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

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Query Match 100.0%; Score 414; DB 2; Best Local Similarity 100.0%; Pred. No. 3.8e-92; Matches 414; Conservative 0; Mismatches 0;
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> AAQ70128 standard; cDNA; 414 25-MAR-2003 14-FEB-1995 AAQ70128; RESULT 2

(first entry) Antimicrobial Rs-AFP1. (revised)

Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.

Raphanus sativus.

21-JUL-1994

WO9416076-A1

94WO-GB000012. 05-JAN-1994;

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Plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFPI from R. sativus. The full-length CDNA sequence of Rs-AFPI is given in AAQ70128. (Updated on 25-MAR-2003 to correct PM field.)
                                                                                                                                                                     Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                Disclosure; Page 31; 39pp; English.
  93GB-00000281
                                                                         Dubock AC, Powell KA,
                                                                                                                WPI; 1994-249223/30.
                                  (ZENE ) ZENECA LID
                                                                                                                                    P-PSDB; AAR57325.
08-JAN-1993;
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ö 61 GTTCTTTTGCTGCTGTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120 180 180 300 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 1120 181 AACCTTGAGAAAGCACGACGAGGATGTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAGTGTATC 240 recractificcircritatriatriccaaactriricgreaatatriritatriatatriac 300 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 121 CCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 1 GITTIATTAGTGATCATGCCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTT 0; Gaps 414 Length 414; Indels 100.0%; Score 414; DB 2; 100.0%; Pred. No. 3.8e-92; iive 0; Mismatches 0; Matches 414; Conservative Local Similarity 121 301 Query Match 61 361 361

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AAT72333 standard; cDNA; 414 BP (first entry) (revised) 25-MAR-2003 19-JAN-1998 AAT72333; RESULT 3 AAT72333

Antifungal protein, candida, fungal resistance, food additive, radish, crop protection, plant defensin, bacterial protection, preservative, ss. Raphanus sativus antifungal protein I (Rs-AFP1) cDNA

Raphanus sativus. 

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241 TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This cDNA clone codes for the preprotein for radish antifungal protein I (Rs-AFP1) (AAM19617). Novel antifungal proteins are based on Rs-AFP1, Rs-AFP2 (see AAM19616), Rs-AFP3 and Rs-AFP4, especially those in which Gly9 is repaced by Arg, Val3b by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by Met. Mutants (see AAW26371-90) of Rs- AFP2 are specifically claimed. The mutants show improved salt tolerant antifungal activity, particularly
                                     ACAAAATAAGTCAGTGACTATCCATGAGTGATTTTTAAGACATGTACCAGATATGTTAT
                                                                          301 ACAAAATAAGTCAGTGACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents.
                                                                                                               Rs-AFP1; radish antifungal protein 1; fungicide; salt tolerance; preservative; transgenic plant; crop protection.
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*tag= a
/rrans1 except= (pos:85. .87, aa:Glu)
16. .102
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100.0%; Pred. No. 3.8e-92;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                       Radish antifungal protein 1 (Rs-AFP1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rees SB;
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                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                                                                                           AAT68696 standard; cDNA; 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This cDNA sequence encodes an Rhapanus sativus (radish) antifungal protein (Rs-AFP1). Analogues of the homologous protein, Rs-AFP2 (AMM19281), have also been produced (see AAM19282-92, AAM19284-98, AAM193101-04, AAM193101-34 and AAM31765-6314). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease tolerance of crops, either pre or post harvest. When applied to plants they may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorganism capable of expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GITCITITITGCIGCITITCGAAGCACCAACAAIGGIGGAAGCACAGAAGIIGIGCGAAAGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTTATGTAATTTAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Borremans FAM, Rees SB;
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100.0%; Pred. No. 3.8e-92;
ive 0; Mismatches 0; Indels
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                                                      .87, aa:Glu)
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/product= "antifungal_protein_1"
                                                      (pos:85.
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Location/Qualifiers
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96GB-00006552.
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nes 414; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-332786/30.
P-PSDB; AAW19280.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Van Gelder WMJ;
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as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well
                     GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
                                                                                                                                            AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC
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                                                                                          121 ccaagregeacaregreacagrereregeaaacaaraacearecaagaareagrecarr
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                                                            CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 composite disease resistance, pathogenic bacteria;
rice white laaf blight, brown-stribe disease, glume blight,
seedling damping-off disease, filamentous fungi, rice blight,
sheath blight disease, leaf blight, gene, ds.
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P-PSDB; ADC51222.
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                                                                               Match 78.2%; Score 323.8; DB 9; Length 394; Local Similarity 90.4%; Pred. No. 5.6e-70; es 357; Conservative 0; Mismatches 37; Indels 1;
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                                                                                           .6e-70;
es 37; Indels
                                                    Seguence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;
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Isolated DNA from Raphanus sativus used to transform a microbe and a plant to produce an antibacterial protein used to increase resistance rice paddy against pathogenic microbes.
                                                                                                                                                                                             The present sequence encodes an antibacterial protein, designated radishin, isolated from Raphanus sativus (radish). A phage or plasmid comprising radishin can be used for increasing resistance of paddy and rice blast disease against pathogenic microbes
                                                                                                                                                                     Claim 1; Page 4; 7pp; Japanese.
                  98JP-00288472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                            Best Local Similarity 81.0
Matches 333; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ38652 standard; DNA;
                                                                        2000-389821/34
                                              (TOYA-) TOYAMA KEN
                                                                       WPI; 2000-389821,
P-PSDB; AAY91117
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                  09-OCT-1998;
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                          Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
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                                                                                                        The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to disease caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                           61 TTCGAGGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAGAGGACCAAGTGGGGACATGG
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pathogenic microbe; radish; rice blast disease; ds.
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                                                                                                                                                                                                                                                                             Length 426;
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                                                                                                                                                                                                                                                  Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                                                            74.3%; Score 307.8; DB 9 88.8%; Pred. No. 4.9e-66; ive 0; Mismatches 42
                                                                              Claim 3; SEQ ID NO 3; 34pp; Japanese.
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Best Local Similarity 88.8 Matches 356; Conservative
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                                                                                                                                                                                                                                                                        64 CITITIGCIGCITICGAAGCACCAACAAIGGIGGAAGCACAGAAGTIGIGGAAAGGCCA
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                                                                                                                Gaps
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                                                        Length 449;
                                                     Score 255; DB 3; Length 44
Pred. No. 4.7e-53;
0; Mismatches 74; Indels
Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;
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81.0%;
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us-10-006-252a-19.rng

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This cDNA represents the sequence of Rs-AFP2 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ3641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to camino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 123bp product, which was further reamplified with the same primers and digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII CDNA library by in situ placed hydridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage their size compared by agarose gel electrophoresis. Four clones had inserts sizes of approx. 400bp the others between 250-300bp. The inserts of the 4 largest clones were then sequenced and found to differ only in the length of their S' and 3' UTK's. The longest sequence was identified as Rs-AFPI (AAQ38650). Rs-AFP2 was seen to differ by only 2 amino acids nucleotide sequence by PCR assisted site directed mutagenesis. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                              Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial diseases.
                                                                                                                                                                                                                                            Terras FRG;
                                                                                                                                                                                                                                            Rees SB,
                                                                                                                                                                                                                                            Cammue BPA, Osborn RW,
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Matches 256; Conservative
/*tag=
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                                                                                                                                                                                                                                                               Vanderleyden J;
                                                                                                                                                                                                                                          Broekaert WF,
                                                                                                      27-AUG-1992;
                                                                                                                                      29-AUG-1991;
                                                                                                                                                                         25-JUN-1992;
                                 WO9305153-A1
                                                                                                                                                        13-FEB-1992;
                                                                   18-MAR-1993
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                                                                                                                                                                      GITITATIAGIGATICATGGCTAAGITITGCGTCCATCATCGCACITCTTTTTGCTGCTCTT 60
                                                                                                                                   GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTTGCTGCTCTT 60
                                                                                          Gaps
                                                                                        ;
0
                                      61.4%; Score 254.2; DB 2; Length 261; 98.8%; Pred. No. 6.5e-53; ive 0; Mismatches 3; Indels 0;
Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;
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                                                                                                                                                                                             Antimicrobial, Rs-AFP2; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; PCR; polymerase chain reaction; mutagenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFP1 from R. sativus. The full-length CDNA sequence of PCR assisted sire-directed mutagenesis of Rs-AFP2 is given in AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rees SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                   94WO-GB000012.
                                                                                                                                                                                                                                                                                                                                                                                                                      93GB-00000281.
                                 AAQ70130 standard; cDNA; 288
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 256; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dubock AC, Powell KA,
                                                                                                         (revised)
                                                                                                                                                              Antimicrobial Rs-AFP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-249223/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                         Raphanus sativus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR57327
                                                                                                                                                                                                                                                                                                                                                                                   05-JAN-1994;
                                                                                                         25-MAR-2003
14-FEB-1995
                                                                                                                                                                                                                                                                                                                                                21-JUL-1994.
                                                                      AA070130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
RESULT 9
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191 AACCTTGAGAAAGCACGACATGGAACTATGTCTTCCCAGCTCACAAATGTATC 250
                                                            241 TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300
                                                                                                                                                                               311 CTATTAAATAAGTATGTGTCACTCTATGAGAGGTCTTATGACATGTACCAGATATGTTAT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein adversely and the antifungal protein 2 (RsAFD2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprocein is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acide A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
protein expression; plant defensin; RSAFP2; antifungal protein; AFP2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.
                                                                                                251 TGCTACTTCCCATGTTAATCTACCAAGAGCTCTTAATGATTATAAAGTGTGTATTT
                                                                                                                                          301 ACAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
3..566
3..562
A. Stags a
/product= "fusion protein of DmAMP1 and RSAFP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evans IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding a fusion protein of DmAMP1 and RSAFP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Bolle MFC,
                                                                                                                                                                                                                                                           371 Grigcrirgrirrahrahggrahacrir 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 34; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Francois IEJA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-GB002716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98GB-00018001
98GB-00026753
                                                                                                                                                                                                                                                                                                                                                           AAZ99339 standard; DNA; 575
                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-246564/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY84072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dahlia merckii.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200011175-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Broekaert WF,
                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .8-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                   AAZ99339;
                                                                                                                                                                                                                     361
                                                                                                                                                                                                                                                                                                                        RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GITITICITIGETGETCETGAAGCACCGAIGGTGGAGGAAGCACAGAAGTIGIGGG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 CCAAGTGGGACATGGTCCGGAGTTGCGGAAACAGTAACGCGTGCAAGAATCAGTGCATT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GITCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGGTCACAAGTGTATC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence encodes the Arabidopsis PDF1.1 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmenate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTATAAACAATAGTCATGGCTAAGTCTGCTACCATCGTTACTCTTTTCTTCGCTGCTCTT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manners JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                  PDF1.1, protection; plant; pathogen; jasmonate; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Terras FRG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7e-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penninckx IAMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 242.4;
Pred. No. 5.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "plant defensin"
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           "PDF1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 72pp; English.
                                       AAV10632 standard; DNA; 403 BP.
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76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96GB-00013753,
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                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                      .6.
/*tag=
.113
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                                                                                                                                                                                                                                                                                                                                                                                                                        *tag=
                                                                                                                                                           A. thaliana PDF1.1 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene from Arabidopsis.
                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-086663/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZENE ) ZENECA LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW40345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Broekaert WF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9800023-A2
                                                                                                                   23-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JAN-1998.
                                                                                                                                                                                                                                                                                                                                                         sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                  Defensin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                             AAV10632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
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Ray JA;

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64 80

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184

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                                                                                                                                                                                                                                                                                    ACGICCCAIGITAAAICTACCACTAAICITIGGIGCIAAAICGIGIGIAITITACAIAAA 320
                                                                                                                                                                                                                                                                                                                   TTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCT 244
                                                                                                                                                                                                                                                                                                                                                                 245 ACTITICCTIGITAATITATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTACACAA 304
                  This sequence encodes the Arabidopsis PDF1.2 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensing gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                                                                                                                           1 TATTAATCATCATCATCGCTAAGTTTGCTTCCATCATCACCTTATCTTCGCTGCTCTTGTTC
                                                                                                                                                                                                                                                                    GTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAAACC
                                                                                                                                                                                                                                                                                                                                TTTTGCTGCTTTCGAAGCACCACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAA
                                                                                                                                                                         5 TATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTC
                                                                                                                         53.9%; Score 223; DB 2; Length 400; 79.9%; Pred. No. 3.3e-45; Indels ive 0; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       AATAAGTCNCTGTCAC - TCTNTGAGTAACTTTATGACATGCA 361
                                                                                                    Sequence 400 BP; 109 A; 82 C; 80 G; 125 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                               AATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTA
Disclosure, Fig 1; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT94581 standard; DNA; 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                             Query Match 53.9
Best Local Similarity 79.9
Matches 274; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shah D, Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-503109/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9737024-A2
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                                                                                                                                                                                                                                                                      125
                                                                                                                                                                                                                                                                                                                     185
                                                                                                                                                                                                                                                                                                                                                                                           261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.
                                                                                                     GCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGGTTGTGCGAAAGGCCAAGTGGG 129
                                                                                                                                                   GCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCCCAAAGGCCAAGTCGT 437
                                                                                                                                                                            130 ACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAG 189
                                                                                                                                                                                             AAAGCACGACATGCATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTT 249
                                                                                                                                                                                                                                      Manners JM;
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;
                                                          ;
0
                                 Length 575
            Seguence 575 BP; 133 A; 137 C; 149 G; 156 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRG,
                                                                                 10 GIGAICAIGGCIAAGIIIGCGICCAICAICGCACIICIIIIIGCIGCI
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Terras
                                   DB 3;
                                / Match 56.1%; Score 232.4; DB 3 Local Similarity 95.6%; Pred. No. 1.8e-47; Nes 239; Conservative 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penninckx IAMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32. .119

/*tag= b

120. .271

/*tag= c

/product= "PDF1.2"

/note= "plant defensin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
32. .274
                                                                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                         DNA; 400
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                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                        CCTTGTTAAT 259
                                                                                                                                                                                                                                                                                              CCTTGTTAAT 567
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                                                                                                                                                                                                                                                                                                                                                                                                                              PDF1.2 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thomma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-086663/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIO.
                                                                                                                                                                                                                                                                                                                                                         AAV10633 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW40346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ZENE ) ZENECA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Broekaert WF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9800023-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                              A. thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
                                                                                                                               70
                                                                                                                                                    378
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                                                                                                                                                                                                                           190
                                                                                                                                                                                                                                                 498
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                                                                                                                                                                                                                                                                                               558
                                                                                                                                                                                                                                                                                                                                                                                 AAV10633
                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kazan K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fund;
                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                 RESULT 12
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Composite cDNA sequence for Alyssum species antifungal polypeptide.
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                                                                                                                                                                                                                                                                Antifungal polypeptide; AlyAFP; inhibition; transgenic plant; phytopathogenic fungus; resistance; ss.
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BP
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              30-APR-1998;
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01-MAR-2000
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                                                                                                                                                                                                                                                                                 126 TGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCT 185
                                                                                                                                                                                                                                                                                                                                 186 TGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTA 245
                                                                                                                                                                                                                                  66 TTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAG 125
                                                                                                                                                                                                                                                                                                                                                         239 rdanagaddaganchcganchriccanchrichtchchchchchanngharrichna 298
                                                                                                                                                                                                                                                                                                                                                                                  CITICCITGITAATITATCGCAAACICITIGGIG-------AATAGITITT 289
                                                                                                                                                                                                                                                                                                                                                                                                         299 CITCCCATGTTAATCTACCAAATCACTTTTTGTGCTTGTGTGTATTTTACATGTTATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                 290 ATGTAATTTACACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACC 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 IGTITATITACATGAATAAGICIGIGICA-ICCTIAIGGGIGACCITATGACAIGIACC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 AGATATGTTAT-----GTTGGTTCGGTTATACAAATAAAGTTTTATTCACCAA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the cDNA sequence encoding the antifungal polypeptide AlyAFP, from plants of the genus AlyBssum. The sequence represents a composite of the sequences isolated by 5, and 3' RACE (Rapid Amplification of cDNA Ends) methods (see AAT94577 and AAT94580). The AlyAFP polypeptide can be used to control phytopathoganic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic fungi
                                                                                                                                                                                                                                                                                                       TGGAACATGGTCAGGCGTGTGTGGGAATAATAACGCATGCAGGAACCAATGCAGAAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wasabia japonica antibacterial protein encoding cDNA SEQ ID NO:1.
                                                                                                                                 49.1%; Score 203.4; DB 2; Length 500; ilarity 72.5%; Pred. No. 2.3e-40; Conservative 0; Mismatches 91; Indels 29,
                                                                                                                                                                                 6 ATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGC
                                                                                                         Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;

    243
    *tag= a
    /product= "antibacterial protein"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ39123 standard; cDNA to mRNA; 414 BP.
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                                                                                                                                           Similarity
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01-MAR-2000
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TCAGGAGTCTGTGGAAACAATGCGTGCAAGAATCAGTGCATCAACCTTGAGGGAGCA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                           An antibacterial protein gene of Wasabia japonica - useful as a food- or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 ITCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TTTGAAGCACCATCAATGGTGGAAGCGCAGAAGTTGTGGGAAAGTCAAGTGGGGACATGG
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Pred. No. 3.5e-40;
0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 414 BP; 108 A; 79 C; 80 G; 147 T; 0 U; 0 Other;
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/product= "antibacterial protein"
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                                                                                                                                                                                                                                                                                                                        Claim 3; Page 12-13; 16pp; Japanese.
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98JP-00121303.
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Best Local Similarity 88.4%;
Matches 220; Conservative
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(first entry)
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                                                                                                                           WPI; 2000-057353/05
                                                          (IWAT-) IWATE KEN.
                                                                                                                                                          P-PSDB; AAY57564
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XX WPI; 2000-057353/05.

DR P-PSDB; AAY57565.

XA An antibacterial protein gene of Wasabia japonica - useful as a food- or PT feed-additive.

XX C Taim 3; Page 13-14; 16pp; Japanese.

XX C The present sequence encodes an antibacterial protein isolated from CC Wasabia japonica. The antibacterial protein can be used as a food or feed CC additive. (Updated on 15-SEP-2003 to standardise OS field)

XX Sequence 416 BP; 111 A; 77 C; 81 G; 147 T; 0 U; 0 Other;
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ö 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195 121 TCAGGAGTCTGTGGAAACAACAATGCGTGCAAGCATCAGTGCATCAACCTTGAGGGAGCA 180 196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255 Query Match 48.6%; Score 201; DB 3; Length 416; Best Local Similarity 88.0%; Pred. No. 8.6e-40; Matches 219; Conservative 0; Mismatches 30; Indels 0; Gaps 256 TAATTTATC 264 241 TAATTATTC 249 qq දු ද à 8 8 8 ò ò

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GenCore version 5.1,6
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US-08-277-192-58

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US-08-277-103-49-16

US-09-103-489-17

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US-09-23-381D-14

US-08-67-706-5

US-09-103-489-14

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Sequence 50, Appl Sequence 8, Appli Sequence 8, Appli Sequence 11, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 20, Appli		un
28 129.8 31.4 284 1 US-08-777-192-50 29 129.8 31.4 284 3 US-08-971-982-50 30 104.2 25.2 306 1 US-08-627-706-8 31 104.2 25.2 306 3 US-08-103-189-8 33 74.6 18.0 243 4 US-09-103-189-8 34 50.8 12.3 150 1 US-08-77-192-34 35 50.8 12.3 150 1 US-08-77-192-34 36 50.8 12.3 150 1 US-08-77-192-34 37 50.8 12.3 150 1 US-08-77-192-34 38 50.8 12.3 150 1 US-08-77-192-34 40 50.6 12.3 50 3 US-08-971-982-34 41 47.6 11.5 150 3 US-08-77-192-31 43 47.6 11.5 150 3 US-08-77-192-31 44 39.6 9.6 1318 4 US-09-71-982-31 45 50.8 12.3 50.8 10.9 0.9 0.9 10.9 0.9 0.9 10.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9	ALIGNMENTS	RESULT 1  US-08-177-687-48  Sequence 48, Application US/08377687  Patent NO. 5538525  GREAL INPORANTION: APPLICANT: BROEKLERT, WILLEM F. APPLICANT: CAMMUE, BRUNO P.A. APPLICANT: CAMMUE, BRUNO P.A. APPLICANT: TERES, SARHE B. APPLICANT: TERES, SARHE B. APPLICANT: TERES, SARHE B. APPLICANT: TERES, SARHE B. APPLICANT: TERES, SARHE B. APPLICANT: TERES, SARHE B. APPLICANT: USA CUSHWAN DARBY & COMPUTER READABLE FORM: MEDIUM TYPE: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PREDICATION DATA: APPLICATION NUMBER: US/08/17,687 TILING DATE: US/08/170N: 16,773 REBERRICE/DOCKET NUMBER: 16,773 REBERRICE/DOCKET NUMBER: 16,773 REBERRICE/DOCKET NUMBER: 16,773 REBERRICE/DOCKET NUMBER: 16,773 REBERRICE/DOCKET NUMBER: 16,773 REBERRICE/DOCKET NUMBER: 16,773 REBERRICE/DOCKET NUMBER: 16,773 REBERRICE/DOCKET NUMBER: 16,773 REGISTRATION NUMBER: 16,773 REBERRICE/DOCKET NUMBER: 1867 TELLEPHONE: 202-61-300 TELLEPHONE: 202-6

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INFORMATION FOR SEQ ID NO:
                                                                                                                           NAME/KEY:
LOCATION:
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                                                                                                              FEATURE:
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                                                                               1 GITTIATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTT
                                                                                                              1 GITITATIAGIGATCATGGCTAAGTITGCGTCCATCATCGCACTTCTTTTGCTGCTCTT
                                                  Gaps
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                  Length 414;
                                                 0; Indels
                    100.0%; Score 414; DB 1; L
100.0%; Pred. No. 7.4e-107;
ive 0; Mismatches 0;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99042/SEE.36525/US/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUND P.A.
APPLICANT: CAMMUE, BRUND P.A.
APPLICANT: TERES, SARAH B.
APPLICANT: TERES, SARAH B.
APPLICANT: TERES, FRANKY R.G.
APPLICANT: VAUDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIPICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 99042/SEE.3
TELEPHONE: 202-861-3003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 48, Application US/08777192; Patent No. 5824869
                    Query Match 100.
Best Local Similarity 100.
Matches 414; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20005
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/971,982

PILING DATE: 17-NO. 6187904-1997
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100.0%; Pred. No. 7.4e-107;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REES, SARAH B.
TERRAS, FRANKY R.G.
VANDERLENDEN, JOZEF
TITLE OF INVENTION: BICCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 48, Application US/08971982
Sequence 48, Application US/08971982
Patent No. 6187904
GENERAL INFORMATION:
APPLICANT: BROBKAERT, WILLEM F.
CAMMUE, BRUNO P.A.
OSBORN, RUPERT W.
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: uncleic acid
STRANDEDNESS: both
TOPOLLGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 414; Conservative
                                                                                                                                    CDS
16..255
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9

Gaps

240 240

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61 GTTCTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGGCGAAAGG 120
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                                                                                                                                                                100.0%; Score 414; DB 4; L. 100.0%; Pred. No. 7.4e-107; ive 0; Mismatches 0;
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FILE REPERENCE: 109946-257 (SWN-035)
CURRENT APPLICATION NUMBER: US/09/077,948A
CURRENT FILING DATE: 1998-08-07
PRIOR PELLING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-03-28
PRIOR FILING DATE: 1996-03-28
PRIOR FILING DATE: 1996-03-28
PRIOR FILING DATE: 1995-12-13
NUMBER: OF SEQ ID NOS: 141
SOUTHARE: FESTERO FOR WINDOWS VERSION 4.0
SEQ ID NO 45
LENGTH + 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 45, Application US/09077948A Patent No. 6605698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: De Samblanx, Genoveva
APPLICANT: Sititema, Lolke
APPLICANT: Meloen, Robbert
APPLICANT: Puijk, Wouter
APPLICANT: Schaaper, Wilhelmus
APPLICANT: Brockaert, Willem
APPLICANT: Van Gelder, Willem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Amerongen, Aart
Fant, Franky
Borremans, Frans
  ; NUMBER OF SEQ ID NOS: 77
; SOFWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Raphanus sativus
US-09-077-951-19
                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 414; Conservative
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ORGANISM: Raphanus sativus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 414; DB 3; Length 414; Best Local Similarity 100.0%; Pred. No. 7.4e-107; Matches 414; Conservative 0; Mismatches 0; Indels
      PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-2NA-1993
ATTORNEY AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRANION NUMBER: 16,773
TELECOMMUNICATION INFORMATION:

TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: De Samblanx, Genoveva
APPLICANT: De Samblanx, Genoveva
APPLICANT: Brockaert, Willem
APPLICANT: Reces, Sarah
ITILE OF INVENTION: Antifungal Proteins
FILE REFERENCE: PPD50093
CURRENT APPLICATION NUMBER: US/09/07,951
CURRENT FILING DATE: 1999-03-11
BARLIER FILING DATE: 1995-12-13
BARLIER FILING DATE: 1995-12-13
BARLIER FILING DATE: 1996-12-13
                                                                                                                                                                                                                                                                                                                                                                          , NAME/KEY: CDS
; LOCATION: 16..255
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-971-982-48
CLASSIFICATION: <Unknown>
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Patent No. 6372888
                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: cDNA
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US-09-077-951-19
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US-09-077-948A-45

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                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AACCTIGAGAAAGCACGACATGGATCTIGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 IGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300
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                                                                                                                                    1 GTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT
                                                                                                    1 GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT
                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 414; DB 4; Length 414; 100.0%; Pred. No. 7.4e-107; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTEY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 58, Application US/08377687
; Sequence 58, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: CAMMUE, BRUNO P. A. APPLICANT: CAMMUE, BRUNO P. A. APPLICANT: CAMMUE, BRUNO P. A. APPLICANT: TERES, SARAH B. APPLICANT: TERES, SARAH B. APPLICANT: TERES, FRANKY R.G. APPLICANT: VANDERLEYDEN, JOZEF TITLE OF INVENTION: BIOCIDAL PROTEINS NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DADRESSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CUSHWAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                     Matches 414; Conservative
     Query Match
Best Local Similarity
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US-08-377-687-58
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61 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 AGACTIGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATGT 267
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                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                               Score 254.2; DB 1; Length 288; Pred. No. 3.9e-62; 0; Mismatches 3; Indels 0.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODRALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: TERES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
ITILE OF INVENTION: BLOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-0AN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/777,192 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 58, Application US/08777192
Patent No. 5824869
GENERAL INFORMATION:
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                          58:
                                                                                                                                                                                                                                                                                                 61.4%;
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: nucleic.acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                          Matches 256; Conservative
                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA
PEATURE:
                                                                                                                                                                                                                               43..282
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Best Local Similarity
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                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: 43...
US-08-377-687-58
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ZIP: 20005
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121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
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| Patent NO. 5773696
| Patent NO. 5773696
| GENERAL INFORMATION:
| APPLICANT: Liang, Jihong
| APPLICANT: Shah, Dilip M. APPLICANT: Wu, Yonnie S. APPLICANT: Mu, Yonnie S. TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi; NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS: 19 CORRESPONDENCE ADDRESS: 19 CORRESPER: 700 Chestefield Village Parkway No. 5773696th
| CITY: St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 288;
                                     NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773
REPERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPKX: 202-861-3000
TELEFXX: 202-861-3000
TELEFXX: 202-861-3000
TELEFXX: 203-861-361
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base, pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: PETCOMPATIBLE
COMPUTER: PETCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
CLASSIFICATION: 436
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; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-08-971-982-58
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                       ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.8
Matches 256; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                      FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AACCTTGAGAAAAGCACGACATGGATCTTGCAACTATGTCTTCCCCAGCTCACAAGTGTATC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 GTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 AGACTTGAGAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCAAGTGTATC 267
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                                                                                                                                                                                                                                                                                                                                                                            Length 288;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U8/08/971,982
FILING DATE: 17-No. 6187904-1997
CLASSIFICATION: <unknown.>
                                                                                                                                                                                                                                                                                                                                                                       61.4%; Score 254.2; DB 1;
98.8%; Pred. No. 3.9e-62;
              99042/SEE.36525/US/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COBORN, RUPERT W.
REES, SARAH B.
TERRAS, FRANKY R.G.
VANDERLEYDEN, JOSEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: SO
CORRESPONDENCE ADDRESS:
ADDRESSE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY.
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/002,480 FILING DATE: 04-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 58, Application US/08971982
Patent No. 6187904
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
CAMMUE, BRUNO P.A.
OSBORN, RUBERT W.
REFERENCE/DOCKET NUMBER: 9904
TELECOMOUNICATION INFORMATION:
TELEPHONE: 202-81-300
TELEPAX: 202-82-094
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDENESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TGCTACTTTCCTTGTTAAT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 İGCİACİTİCCİİGİLAAİ 286
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ZIP: 20005
COMPUTER READABLE FORM;
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                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.8
Matches 256; Conservative
                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                     43..282
                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: 43...
US-08-777-192-58
                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 CCATCAGGGACTIGGICAGGAGTCTGCGGAACAACGACGATGCAAGGAACCAATGCATC 195
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Patent No. 6215048

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shah, Dilip M.
APPLICANT: Why Younie S.
APPLICANT: Wow Younie S.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      52.9%; Score 219; DB 1; Length 285; 90.3%; Pred. No. 2.8e-52; Indels tive 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Charles E. Cohen, Monsanto Company, BB4F 700 Chesterfield Village Parkway No. 6215048th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYGTHER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMER: US/09/103,489
FILING DATE: 24-UUN-1998
CLASSIFICATION: 800
                                                                          38-21 (10700) A
                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "synthetic DNA"
US-08-627-706-16
            REGISTRATION NUMBER: 34,565
REGISTRATION NUMBER: 34,565
RELECOMMUNICATION INVORMATION:
TELEPONE: (314)537-624
INPORMATION FOR SEQ ID NO: 5SQUENCE CHARACTERISTICS: LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
ATTORNEY/AGENT INFORMATION: NAME: Cohen, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 90.3
Matches 234; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
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STATE: Missouri
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US-09-103-489-16
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Sequence 16. Application US/09829381D

Sequence 16. Application US/09829381D

Ratent No. 6652280

GENERAL INFORMATION:
APPLICANT: Liang, Jihong

APPLICANT: And, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Plant Pathogenic Fungi
FILER REFERENCE: 32 = 21 (10700) C

CURRENT APPLICATION NUMBER: US/09/829,381D

FILER REPERENCE: 32 = 201-04-09

PRIOR PILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1

SEQ ID NO 16

ENERGY 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                         52.9%; Score 219; DB 3; Length 285; 90.3%; Pred. No. 2.8e-52; Indels iive 0; Mismatches 25; Indels
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REFERENCE/DOCKET NUMBER: 38-21 (10700) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6274
TELEPHONE: (314) 537-6047
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHRAACTENISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOCHOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 90.3
Matches 234; Conservative
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US-09-829-381D-16
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121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
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DESCRIPTION: /desc = "synthetic
US-09-103-489-17
                                                                                                                                                                                                                                                                                                                                             ; Sequence 17, Application US/09103489; Patent No. 6215048; GENERAL INFORMATION:
                                                                                                                                                                                                   241 IGCTACTTICCTTGAAT 259
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                         US-09-103-489-17
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GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
                                                                                 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATGAGTGCATT 180
                                                                                                                                                                181 AACCTTGAGAAAGCACGACATGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
                                   GTTCTCTTTGCTGCTTTCGAGGCACCAACTATGGTGGAGGCACAAAAGTTGTGCGAGAGG 135
                                                                                                                      CCATCAGGGACTTGGTCAGGAGTCTGCGGAAACAACAAGGATGCAAGGAACCAATGCATC 195
                                                                                                                                                                                              61 GTTCTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
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Fatent No. 5773696
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CUDNIKE: USA

CUP. 13198

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/627,706
FILING DATE:
CLASSIPICATION: 436
ATTORNEY AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34.565
REFERENCE/DOCKET NUMBER: 38-21 (10700) A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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DESCRIPTION: /desc = "synthetic DNA"
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 89.6
Matches 232; Conservative
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196 AGACTCGAGAAGGCACGGCATGGATCTTGCAACTACGACTTCCCAGCTCACAAGTGCATC 255
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                                                                             181 AACCTTGAGAAAGCACGACGACATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Row, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Date Ploppy disk
COMPUTER: Date Ploppy disk
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APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UN-1998
CALESCIPION: NUMBER: 34.565
REFERENCE COMPUTION NUMBER: 34.565
REFERENCE (314) 537-624
TELEPHONE: (314) 537-624
TELEPHONE: (314) 537-624
TELEPHONE: (314) 537-647
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
TRANGTH: 285 base pairs
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239 TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTA 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 ITITICCICCITICCAACCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 CTTTGCTGCTTTTGAAGCACCAGCAATGGTGGAGTCACGGAAGTTGTGCGAGAGTCCAAG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 TGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 TGGAACATGGTCAGGCGTGTGGGAATAATAACGCATGCAGGAACCAATGCAGAAGCT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 TGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTA 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.5%; Pred. No. 8.4e-48;
Matches 317; Conservative 0; Mismatches 91; Indels 29
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSES CARLES E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
                                                                                                                                                                                              COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 38-21(10700)A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: May 13, 2004, 10:54:47
                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398 AAAAAAAAAAAAAAA 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (314) 537-6224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                 CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                                        63198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Job time : 85 secs
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APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Younde S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Contro TITLE OF INVENTION: Plant Pathogenic Fungi
FILE OF INVENTION: Plant Pathogenic Fungi
CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT FILING DATE: 2001-04-09
PRIOR PLILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Batentin version 3.1
LENGTH: 285
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181 AACCTTGAGAAAGCACGACGACGATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
                                                                                         196 AGACTCGAGAAGGCACGCCATGGATCTTGCAACTACGTCTTCCCAGCTCACAAGTGCATC 255
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Patent No. 5773696
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09829381D Patent No. 6653280 GENERAL INFORMATION:
                                                                                                                                                     241 IGCTACTITCCTIGIDAT 259
                                                                                                                                                                              256 TGCTACTTTCCATGCTAAT 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic US-09-829-381D-17
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US-08-627-706-9
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1: /cgr12_6/ptodate12/pubpna/USO7_PUBCOMB.seq:*
2: /cgr12_6/ptodate12/pubpna/PCT_NEW_PUBL.seq:*
3: /cgr12_6/ptodate12/pubpna/PCT_NEW_PUBL.seq:*
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6: /cgr12_6/ptodate12/pubpna/USO8_NEW_PUB.seq:*
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11: /cgr12_6/ptodate12/pubpna/USO8_PUBCOMB.seq:*
11: /cgr12_6/ptodate12/pubpna/USO8_NEW_PUB.seq:*
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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% Query Match Length DB	414	414	414	288	403	400	400	285	285	285	285	500	500	243	
* Query Match	100.0	100.0	100.0	61.4	58.6	53.9	53.9	52.9	52.9	52.1	52.1	49.1	49.1	47.5	
Score	414	414	414	254.2	242.4	223	223	219	219	215.8	215.8	203.4	203.4	196.6	
Result No.	-	7	m	4	'n	9	7	80	თ	10	11	12	13	14	

15   196.6   47.5   243   11   US-09-398-842A-2046   16   194.6   47.0   308   30.90-993-391A-12   194.6   47.0   308   31   US-09-693-391A-14   31   43.5   270   31   US-09-693-391A-14   31   43.5   270   31   US-09-693-391A-14   32   138.4   43.2   286   31   US-09-693-391A-12   22   153.8   43.2   286   31   US-09-693-391A-12   23   153.8   43.2   286   31   US-09-693-391A-12   23   153.8   43.2   286   31   US-09-693-391A-12   23   153.8   31.4   31.5   30.6   31   US-09-693-391A-12   23   104.2   25.2   306   31   US-09-693-391A-13   26   31.2   31.6   30.9   US-09-70-69-293   25.6   31.2   31.6   31.8   31.5   30.6   31.5   31.6   31.5   31.6	
	15 196.6 47.5 243 11 US-09-938-842A-17 194.6 47.0 308 9 US-09-82-381A-195-196 19 US-09-82-381A-195-196 19 US-09-82-381A-195-196 19 US-09-82-381A-195-196 19 US-09-82-381A-195-196 19 US-09-82-381A-195-196 19 US-09-82-381A-195-196 19 US-09-82-381A-195-196 19 US-09-82-381A-195-196 19 US-09-82-381A-196 19 US-09-82-381A-196 19 US-09-75-564-57 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-564-59 19 US-09-75-59 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAACAATAACGCATGCAAGAATCAGTGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATĆAGTGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AACCTTGAGAAAGCACGACGATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AACCTTGAGAAAGCACGACATGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 Techachtrichtanthancecaactchingereaarachtrinangraatinac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 ACAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTTAAGACATGTACCAGATATGTTAT 360
                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTTGCTGCTCTT
                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Van Amerongen, Aart
APPLICANT: Fant, Franky
APPLICANT: Borremans, Frank
APPLICANT: Borremans, Frank
APPLICANT: Sitjtsma, Lolke
APPLICANT: Sitjtsma, Lolke
APPLICANT: Schaaper, Wilhelmus
APPLICANT: Schaaper, Wilhelmus
APPLICANT: Schaaper, Wilhelmus
APPLICANT: Schaaper, Wilhelmus
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: 50094PPDDIV CURRENT APPLICATION NUMBER: US/10/388,361A
CURRENT APPLICATION NUMBER: US 09/077,948
PRIOR APPLICATION NUMBER: PCT/GB96/03068
PRIOR APPLICATION NUMBER: PS PRIOR APPLICATION NUMBER: PS PRIOR APPLICATION NUMBER: BS PRIOR PILING DATE: 1998-08-07
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1998-122
PRIOR FILING DATE: 1998-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 45, Application US/10388361A; Publication No. US20030226169A1
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INPORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: boch
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 414; Conservative
                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 16..
US-09-759-584-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
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                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                        100.0%; Score 414; DB 13; Length 414; 100.0%; Pred. No. 3.3e-101; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 414; DB 14; Length 414; Best Local Similarity 100.0%; Pred. No. 3.3e-101; Matches 414; Conservative 0; Mismatches 0; Indels 0;
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US-10-006-252A-19

Sequence 19, Application US/10006252A

Publication No. US20020152498A1

GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Breckaert, Willem
APPLICANT: Rees, Sarah
ITILE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYV-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT APPLICATION NUMBER: US/10/006,252A

CURRENT APPLICATION NUMBER: GB 9525474.4

PRIOR APPLICATION NUMBER: GB 9525474.4

PRIOR APPLICATION NUMBER: GB 9525474.4

PRIOR APPLICATION NUMBER: GB 9525474.4

PRIOR APPLICATION NUMBER: GB 9525474.4

PRIOR APPLICATION NUMBER: GB 9525474.4

PRIOR APPLICATION NUMBER: GB 9525474.4

PRIOR APPLICATION NUMBER: GB 9525474.4

PRIOR APPLICATION NUMBER: GB 9525474.4

PRIOR APPLICATION NUMBER: GB 9525474.4

PRIOR APPLICATION NUMBER: GB 9525474.4

PRIOR APPLICATION NUMBER: DS 12-12

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 19
                                                         NUMBER OF SEQ ID NOS: 141
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGIH: 414
PRIOR APPLICATION NUMBER: GB 9525455.3
PRIOR FILING DATE: 1995-12-13
                                                                                                                                                                                  TYPE: DNA
ORGANISM: Raphanus sativus
                                                                                                                                                                                                                                                                                                                                                                        Matches 414; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Raphanus sativus
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                  US-10-388-361A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-006-252A-19
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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                                                    ; NAME/KEY:
; LOCATION:
US-09-759-584-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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STATE:
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                                                                61 GITCTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
                                                                                                                                       121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
                                                                                                                                                                                                                                                                                        241 IGCTACTITCCTIGITAATITATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300
                                                                                                                                                                                                                                                                                                                                                              301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
                                                                                                                                                                                                                                                                                                                                                                                      GITCITITIGCIGCITICGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
                                                                                                                                                              AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
                                                                                                                                                                                                                                                   181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
                     241 rgcractriccrigitaaritrarcecaacterriegigaaragrirrrargraarirae 300
CTTTGCTGCTCTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/377,687
FILLING DATE:
ATTORNEY/AGENT INPORMATION:
NAME: XCKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFAX: 202-861-3000
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEACHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BROBKAERT, WILLEM F.
APPLICANT: CANNUE, BRUNO P.A.
APPLICANT: OSBORN, RUBERT W.
APPLICANT: RES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, UOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES. 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 58, Application US/09759584 Patent No. US20010014732A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
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: USA
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88 GITCITITIGCIGCITICGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCCAAAAGG 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 CCAAGTGGGACATGTCGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 AGACTIGAGAAAGCACGACGACGATCTIGCAACTAIGTCTICCCAGCICACAAGIGIAITC 267
                                                                                                                                                                                                                                         87
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                                                                                                                                                                                    1 GITTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT
                                                                                                                                                                                                                                    28 GITITATIAGIGATCAIGGCIAAGITIGCGICCAICAICGACITCTITIGCIGCICIT
                                                                                                                                                                                                                                                                                                                                                                                                 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
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0
                                                                                 Length 288;
                                                                                                                                 Indels
                                                                            61.4%; Score 254.2; DB 9;
98.8%; Pred. No. 2.8e-58;
live 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thomma, Bart
APPLICANT: Terras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Kazan, Kemal
APPLICANT: Broekaert, Willem
IIILB OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: 9PD 50165/UST
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09732561
Patent No. US20020035738A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: ZENECA AG Products
STREET: 1800 Concord Pike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 IGCIACTITCCTIGITAAT 259
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                                                                      Query Match
Best Local Similarity 98.8
Matches 256; Conservative
43..282
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61 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATC 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 CTATTAAATAAGTATGTGTCACTCTATGAGAGGTCTTATGACATGTACCAGATATGTTAT 370
                                                                                                                                                                                                                                                                                                                                                                    11 GTATAAACAATAGTCATGGCTAAGTCTGCTACCATCGTTACTCTTTTCTTCGCTGCTCTTT
                                                                                                                                                                                                                                                                                                                                        1 GITTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                              Query Match 58.6%; Score 242.4; DB 9; Length 403; Best Local Similarity 76.5%; Pred. No. 5e-55; Matches 297; Conservative 0; Mismatches 91; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...DUIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09732561
Patent No. US20020035738A1
GENERAL INFORMATION:
APPLICANT: Thomma, Bart
APPLICANT: Penninckx, Iris
APPLICANT: Razan, Kemal
APPLICANT: Manners, John
APPLICANT: Manners, John
APPLICANT: Brockert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 GTTGGTTCGGTTATACAATAAAGTTTT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 Grigoringrinrahahaksenahacini 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: ZENECA AG Products
1: 1800 Concord Pike
Wilmington
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS; single
                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA ORLEGINAL SOURCE: STRAIN: PDF 1.1
                                                                                                                                        CDNA
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65 TITITIGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAA 124
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APPLICANT: Chang, H.
APPLICANT: Thu, T.
APPLICANT: Wang, X.
APPLICANT: Wang, X.
APPLICANT: Wang, X.
TITLE OF INVENTION: Promoters for regulation of plant expression FILE REFERENCE: 1360.001US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 53.9%; Score 223; DB 9; Length 400; Best Local Similarity 79.9%; Pred. No. 8.2e-50; Matches 274; Conservative 0; Mismatches 67; Indels
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                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, 112a D.
REGISTAATION NUMBER: 33,712
REPERENCE/DOCKET NUMBER: PPD 50165/UST
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 15:
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CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/258,692
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Patent No. US20020144047A1
                   APPLICATION NUMBER: 09/202,638 FILING DATE:
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA ORIGINAL SOURCE: STRAIN: PDF1.2
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Best Local Similarity
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Best Local Similarity
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                           Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SINEEL: 'NO UNBESTITIED VILLAGE PARKWAY NO. USZUG CITY: St. Louis STATE: Missouri COUNTR: St. Louis COUNTR: St. Louis COUNTR: USA ZIP: 63198
COMPUTER READABLE FORM:
MEDIUW TYPE: Ploppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/09/829,381A FILING DATE: 09-Apr-2001 CLASSIFICATION NUMBER: US/09/829,381A APPLICATION NUMBER: 09/103,489 FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                       67; Indels
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                                                                                                                                                                                                                                                                                                                    Score 223; DB 9;
Pred. No. 8.2e-50;
0; Mismatches 67;
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 607
LENGTH: 400
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                     FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(400)

OTHER INFORMATION: n = A,T,C (US-09-887-576-607
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 79.9%;
Matches 274; Conservative
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US-09-829-381A-16
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APPLICANT: Lidang, Jihong
APPLICANT: Lidang, Jihong
APPLICANT: Lidang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for CO
TITLE OF INVENTION: Plant Pathogenic Pungi
TITLE OF INVENTION: Plant Pathogenic Pungi
TITLE OF INVENTION: Plant Pathogenic Pungi
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT PLING DATE: 2001-04-09
PRIOR FILING DATE: 2001-04-09
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.9%; Score 219; DB 9; Length 285; 90.3%; Pred. No. 8.2e-49; ive 0; Mismatches 25; Indels
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-624
TELEPHONE: (314) 537-6047
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 219; DB 13;
Pred. No. 8.2e-49;
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: (Gesc = "synthetic DNA" SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TGCTACTTTCCTTGTTAAT 259
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90.3%;
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ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
                                                    16 GITITATIAGEGAICAIGGCTAAGITIGCGICCAICAICGCACICCICITIGCTGCTCC
                                                                                                61 GITCITITIGCIGCITITCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
Gaps
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APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Wo, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPATURE: LBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION NUMBER: 09/103,489
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
RESPERENCEZ DOCKET NUMBER: 34,565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEPHONE: (314) 537-6047
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
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DESCRIPTION: /desc = "synthetic DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-829-3819-17
 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           TGCTACTTTCCTTGTTAAT 259
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STRANDEDNESS: single
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 234; Conservative
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Query Match

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61 GITCTITITGCTGCTTICGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
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                                                                                            61 GITCITITIGCIGCTITICGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
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Pred. No. 5.9e-48;
); Mismatches 27;
                0; Mismatches
                                                                                                                                                                                                                                                                   241 TGCTACTTTCCTTGTTAAT 259
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89.68;
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  Best Local Similarity 89.6
Matches 232; Conservative
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: W. Yonnie S.
APPLICANT: W. Yonnie S.
APPLICANT: W. Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for CO.
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C.
CURRENT APPLICATION NUMBER: US/10/681, 972
CURRENT FILING DATE: 2001-04-09
PRIOR FILING DATE: 2001-04-09
PRIOR PALICATION NUMBER: 09/103, 489
PRIOR FILING DATE: 1998-06-24
                        350 AGATATGITAT------GITGGITCGGITATACAAATAAAGITITATTCACCAA 397
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1 LOCATION: (22)...(22)
2 OTHER INFORMATION: N = any nucleotide
US-10-681-972-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
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SOFTWARE: Patentin versic
SEQ ID NO 9
LENGTH: 500
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ORGANISM: Alyssum spp
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US-10-681-972-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGGCTCACAAGTGTATCTGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.1%; Score 203.4; DB 9; Length 72.5%; Pred. No. 1.7e-44; Live 0; Mismatches 91; Indels
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REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 TOPOLOGY: linear

7 NOLECULE TYPE: CDNA

7 SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-829-381A-9
                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 317; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: St. Louis
STATE: Missouri
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US-09-829-381A-9
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Sequence 2046, Application US/09938842A
Patent No. US20020166378A1
GENERAL INFORMATION:
APPLICANT: Harper, Joef
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF PLANTS, TRANSGENIC FLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPERANCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TCAGGGGTTTGCGGAAACAGTAATGCATGCAAGAATCAGTGCATTAACCTTGAAGGAGCC 180
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350 AGATATGTTAT-----GTTGGTTCGGTTATACAAATAAAGTTTTATTCACCAA 397
                                    418 AGATATATCATATGTAGTTTGTTGTTGTGGCAATTATAAACTTTTATTGTGGA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAAGTGGGACATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGCTAAGTTTGCTTCCATCATCACCCTTATCTTCGCTGCTCTTGTTCTTTGCTGCT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FLING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR PELLING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                    398 AAAAAAAAAAAAAA 414
                                                                                                                             478 TGCAAAAAAAAAAAA 494
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                                                                                                                                                                                              RESULT 14
US-09-938-842A-2046
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US-09-938-842A-2046
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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AAACATGGATCATGCAACTATGTCTTCCCAGCACAAGTGTATCTGTTACGTCCCATGT 240
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            CURENT FILING NUMBER: US/09/938,842A
CURENT FILING DATE: 2001-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2864
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FILE REFERENCE: SCRIP1300-3
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 458)
Genoplante.
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Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infoblogen.fr).
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Unpublished (2003)
Contact; Genoplante
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     CD834994 BN45.0430
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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/mol type="mRNA"
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7e1: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplance-info.infobiogen.fr).
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Contact: Genoplante
Genoplante
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                                                                                             Length 470;
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                                                                                                                                       38; Indels
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                                                                                             DB 14;
                                                                                             Score 311.2; DB 14
Pred. No. 2.2e-41;
                                                                                                                                          0; Mismatches
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/mol_type="mRNA"
/cultivar="Jet neuf"
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/tissue_type="seed"/clone_lib="BN40"
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/clone_lib="BN45"
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89.7%;
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Brassica napus
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                                                                                          Query Match
Best Local Similarity 89.7
Matches 357; Conservative
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Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Contact: Genoplante
Genoplante
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Location/Qualifiers
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                                                                                   GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
                                                                                                                                                                                           175 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAATCAGGGTTT
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Larity 86.4%; Pred. No. 2.6e-41;
Conservative 0; Mismatches 54; Indels 2;
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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BN40.661003F011227 BN40 Brassica napus cDNA clone BN40061003, mRNA
sequence.
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Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
1el: 31 69 47 54 00
Fax: 33 16 94 75 4 00
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                      121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
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Score 311; DB 14; Length 446;
Pred. No. 2.5e-41;
0; Mismatches 40; Indels 2
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                                                                                   GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTT
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cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BA40061003"
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Best Local Similarity 89.2%;
Matches 347; Conservative
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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BN40.063015F011228 BN40 Brassica napus cDNA clone BN40063015, mRNA
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                                                                                                                                                                CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGGGTG 230
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      GTTCTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
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Contact: Genoplante
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Brassica napus"
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/tissue type="seed"
/clone_lib="BN40"
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CD832592.1 GI:32514532
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Brassica napus
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CD833779 408 bp mRNA linear EST 10-JUL-2003
BN45.001115F010914 BN45 Brassica napus cDNA clone BN45001115, mRNA
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                                                                                   349
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Location/Qualifiers
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Contact: Genoplante
Genoplante
121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
                                                                                                                                                                                                                                                                                       AACCITGAGAAAGCACGACATGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheor
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 408)
Genoplante.
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Pred. No. 4.8e-41;
0; Mismatches 41; Indels 2;
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CD834611 450 bp mRNA linear BST 10-JUL-2003
BN45.042H07F011228 BN45 Brassica napus cDNA clone BN45042H07, mRNA
sequence.
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Brassica napus
Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica
                              301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358
                                                                                                 314 ATAAAATCAGTGTCACTATCAATGAGTGATTTTATGACATGTACCTGATATATGTT 373
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Contact: Genoplante Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
            TGCTACTTTCCTTAATTTATCGCAACTCTTTGGTGAATAGTTTTATGTAATTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 GRATIACTAGTGAGCATGGCTAAGTTTGCTTCCATCATTGCCCCACTTTTTGCTGCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 ccaagregeacaregercaegaercreregaaacaaraacecareraagaarcaerer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GITTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTT
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/clone="BN45042H07"
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/clone_lib="BN45"
                                                                                                                                                ATGTTGGTTCGGTTATACAAATAAGTTT 387
                                                                                                                                                                374 AIGTIGGTICGGTIAIAAAAAAGTITT 402
                                                                                                                                                                                                                                                                                                                  CD834611
CD834611.1 GI:32516551
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                                                                                                                                                                                                                                                                                                                    ## 409 pp #RNA linear EST 10-JUL-2003 BN45.040121F011018 BN45 Brassica napus CDNA clone BN45040121, mRNA sequence.
       240
                                         252
                                                                  TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTTATGTAATTTAC 300
                                                                                        ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358
                                                                                                                                                         Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
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Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr)
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AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC
                           ACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATT
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                                                                                                                                                                                                         ATGITGGTTCGGTTATACAATAAAGTTT 387
                                                                                                                                                                                                                                          ATGTTGGTTCGGTTATAAAAAGTTTT 401
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/db.xref="taxon:3708"
/clone="BN45040121"
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/clone_lib="BN45"
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CD834090.1 GI:32516030
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Brassica napus
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CD834090
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Query Match 74.2%; Score 307; DB 14; Length 420; Best Local Similarity 90.4%; Pred. No. 1.1e-40; Matches 328; Conservative 0; Mismatches 35; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Brassica napus"
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/clone="BN45040B07"
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/clone_lib="BN45"
                                                                                                                                                                                                     CD833944.1 GI:32515884
                                                                                                                                                                                                                                        Brassica napus (rape)
                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                (bases 1 to 420)
                                                                                                                                                                                                                                                         Brassica napus
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Best Local Similarity
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                                       396 GTT 398
 361 GTT 363
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                                                                                                                                                                                                 CD831294 11near EST 10-JUL-2003 BN40.058N13F011019 BN40 Brassica napus cDNA clone BN40058N13, mRNA
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Brassica napus
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales; Brassicaceae, Brassica.
1 (bases 1 to 438)
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Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                        359 ATGITGGITCGGITATACAAATAAAGITT 387
                                                                                                       411 Argircerregerraraaaagriri 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Brassica napus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:3708"
/clone="BN40058N13"
/tissue_type="seed"
/clone_lib="BN40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/cultivar="Jet neuf"
                                                                                                                                                                                                                                                                       CD831294.1 GI:32513234
                                                                                                                                                                                                                                                                                                          Brassica napus (rape)
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Best Local Similarity 90.65
Matches 329; Conservative
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CD833944 EST 10-JUL-2003 MRNA Finear EST 10-JUL-2003 HAS:040B07F011019 BN45 Brassica napus CDNA clone BN45040B07, MRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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                                                  EST 10-JUL-2003
BN25064A05, mRNA
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                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                                                                         Genoplante.

Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                           93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 00
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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                                     BN25.064A05F020416 BN25 Brassica napus cDNA clone sequence.
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                                                                                                                                                                                                                                                                                                                                                                                     organism="Brassica napus"
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/tissue_type="seed"
/clone_lib="BNS5"
                                                                                                  CD826491.1 GI:32508431
                                                                                                                            Brassica napus (rape)
Brassica napus
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AUTHORS
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RESULT 13 CD833983

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CD833983
BN45.040D11F011019 BN45 Brassica napus CDNA clone BN45040D11, mRNA
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Peprantophyta, Magnollophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales; Brassicaceae, Brassica.
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infoblogen.fr),
Location/Qualifiers
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Local Similarity 90.4%; Pred. No. 1.1e-40;
hes 328; Conservative 0; Mismatches 35;
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                                                                               CD833983
CD833983.1 GI:32515923
                                                                                                                                                       Brassica napus (rape)
Brassica napus
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Matches 328; Conservative
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BN40.059J13F011208 BN40 Brassica napus cDNA clone BN40059J13, mRNA
                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                           Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
                                                                                                                                                                                                                                                                                      This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr)
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Best Local Similarity 90.4%; Pred. No. 1.1e-40;
Matches 328; Conservative 0; Mismatches 35; Indels 0; Gaps
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                                                                                                                                                                                                                           93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                 /organism≈"Brassica napus"
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 CD827413.1 GI:32509353
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SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermachyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

    Chases I to 438)

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Contact: Genoplante
Genoplante
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                                                                                                                                                                                                                                                                                                 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tal: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
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